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Listing first 45 summaries
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11192.003 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Qy 241 C	181	Ov 181 A	121	Db 61 6	Qy 61 G	Db . 1 c	Ογ 1 (Query Match Best Local Similarity Matches 2699; Conser	RESULT 1 AR135732 LOCUS LOCUS DEFINITION Seq ACCESSION AR1 VERSION AR1 VERSION IN KEYWORDS Unk ORGANISM Unc REFERENCE 1 AUTHORS LOV TITLE DNA JOURNAL PAT FEATURES BOURCE ORIGIN	
CCCAGCTCTCGGCCGGCGCCCTGCCCGGGTGAGCCGGGTGAGCCTGCGGGGCCAT		DOJEDDOJEDIJE SE STANJENIO DE PRESIDIJE SE STANJENIO PRINTENIO PROGRANJANJENIO NA STANJANJA PROJEKTI NA STANJA	CCGCCTGCTCTGGCCCCGGCCCCCGGCCCCCGGACCATGCGCTGGGCGCCCCCAGGGGAA	GCTGCAGCAGCCGCGCTGCCGGCCCCACTGGGCTCGGATCCGGCCCCGGCCCCCTCGGCA	gcTgcAgcAgcCgggCTgCCgGgCCCCACTGGGCTCCGATCCGGCCCCGGCCCCCTCGGCA	CCACGCGTCCGCCGGCTGCACGGTCGCACCGGCTCAGGGTCCGGCTCCTCTCCC	ccacgcgrcgccagcrgcacggrcgcaccggcagcggcrcaggcrccgcrcrccc	100.0%; Score 2699; milarity 100.0%; Pred. No. 0; Conservative 0; Mismatches	AR135732 2699 bp DNA Sequence 5 from patent US 6136559. AR135732 AR135732.1 GI:14476404 . Unknown. Unknown. Unclassified. 1 (bases 1 to 2699) Lovenberg, T.W., Erlander, M., Huvar, A. and DNA encoding as human histamine receptor Patent: US 6136559-A 5 24-OCT-2000; Location/Qualifiers 1. 2699 /organism="unknown" /mol_type="unassigned DNA"	
CGGAGCCGCGTGAGCCT	CTCCCGGGCCGGGGCCC	JJJDDDDDDDDDDDDJJJDTD	ACCATGCGCTGGGCGCC	rcegarccegccccegc	TCGGATCCGGCCCCGGC	AGCGGCTCAGGCTCCGG	AGCGGCTCAGGCTCCGG	DB 6; Length 0; Indels	linear H Pyati,J.	
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181 ACCCGACCCGGCCAAGGGCCCGCAAAGACGAGGCTCCCGGGGCCGGGGCCCCTCCCGGCCG 240	121 CCGCCTGCTCTGGCCCCGGCCCCGGCCCCGGGGACCATGCGCTGGGCGCCCCCAGGGGAA 180	61 GCTGCAGCAGCCGCGCTGCCGGCCCCACTGGGCTCGGATCCGGCCCCGGCCCCCTCGGCA 120	1 CCACGCGTCCGCCGGCTGCACGGTCGCACCGGCAGCGGCTCAGGCTCCCGGCTCCTCTCCC 60	Query Match 100.0%; Score 2699; DB 6; Length 2699; Best Local Similarity 100.0%; Pred. No. 0; Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/di /ino	FT source 12699 /organism='Artificial Sequence'. EATURES Location/Qualifiers	GO1N33/15,GO1N33/50, PC C12N15/00,A61K37/02,C12N5/00 CC Description of Artificial Sequence: CDNA FH Key Locarion/onalifiers	A61P25/16, PC A61P25/18,A61P25/22,A61P25/24,A61P25/28,C07K14/705,C07K16/28, PC C12N1/15,C12N1/21.C12N5/10.C12P21/02.C12O1/02.C12O1/68.PC	PF 07-OCT-1998 JP 2000573370 PI /TIMOTHY W LABENBERG, MARK ERLANDER, ARNE HUBER, JIYAYASYURY PI PIATEI PC C12N15/09. A61K38/00. A61K45/00. A61P3/04. A61P3/10. A61P9/06. PC	ORTHO MCNEIL PHARMACEUTICAL INC COMMENT OS Artificial Sequence PN JP 2002526049-A/5 PD 20-AUG-2002	REFERENCE 1 (bases 1 to 269) AUTHORS Labenberg, T.W., Erlander, M., Huber, A. and Piatei, J. TITLE Isolated DNA encoding human H3 histamice receptor JOURNAL Patent, JP 2002525649-A 5 20-AUG-2002;	JP 2002526049-A/S. synthetic construct synthetic construct exhibet seconstruct	BD235872 ON Isolated DNA encoding N BD235872		2641 AACCGTGAGGTCACAATAAAGTGTATTTTTTTAAAAAAAA	2581 GTGCACCCGTGCCACGCGCTCTGCATGCTCCTCTGCCTGTGCCCGCTGCGCTGCCCTGCA 2640	2521 CAAGGCGTGCAGGGGCCGGTCCAGAGGAGGCAGGCAGGGGCCGCTTCGCCATGTGCT 2580	2461 GCTCACCCAGGACCTCTGGGGGGTTGTTGGGAGGAGGGGGCCCGGCTGGGCCCGAGGGTCC 2520
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Unclassified.

E 1 (bases 1 to 2699)

E Lovenberg, T.W., Erlander, M., Huvar, A. and Pyati, J.

DNA encoding a human histamine receptor of the H3

(AL Patent: US 6413743 A 5 02-JUL-2002;

Location/Qualifiers

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Oy 361 GGCGGCGGGGGGGGGGCGCGCTCTTCTGGCAGCCTGGACCGCGGTGCTGGCCTCAT 420	Db 181 ACCCGACCCGGCCAAGGGCCCGCAAAGACGAAGCCTCCCGGGCCGGGCCCTCCCGGCCG 240 Qy 241 CCCAGCTCTCGGCCGGCCGCAAAGACGAAGCCTCCCGGGCCGGTGAAGCCTGCGGGGCAT 300	Qy 61 GCTGCAGCAGCCGCGCTGCCGGCCCACTGGGCTCCGGATCCGGCCCCCGGCCCCTCGGCA 120 11	Query Match 100.0%; Score 2699; DB 6; Length 2699; Best Local Similarity 100.0%; Pred. No. 0; Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Y 1 CCACGCGTCCGCCGGCTGCACGGTCGCACCGGCAGCGGCTCCAGGCTCCTCCTCCC 60	JOURNAL Patent: WO 02061087-A 548 08-AUG-2002; Lifespan Biosciences, Inc. (US) FEATURES SOURCE 1. 2699 /organism="Homo sapiens" /mol type="unassigned DNA" ORIGIN /db_xref="taxon:9606"	OKGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P. Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic partides	AX549 Seque AX549 AX549	Db 2581 GTGCACCGTGCCACGGGCTCTGCATGCTCCTCTGCCCGTGCCCCTGCA 2640 Qy 2641 AACCGTGAGGTCACAATAAAGTGTATTTTTTAAAAAAAAA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2699)
Lovenberg, T.W., Roland, B.L., Wilson, S.J., Jiang, X., Pyati, J.,
Huvar, A., Jackson, M.R. and Erlander, M.G.
Cloning and functional expression of the human histamine H3
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3535 General Atomics Ct, San Diego, CA 92121, USA
Location/Qualifiers
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Homo sapiens histamine
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Lovenberg, T.W., Roland, B.R., Wilson, S.J.,
Huvar, A., Jackson, M.R. and Erlander, M.E.
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GGCGGCGGGCGCGCGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCCGCGCTCAT
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PR 04-DEC-1997 US 08/985090,17-WAR-1998 US
ANDREW D J GOODEARL,ALEXANDRA M GLUCKSMANN,MICHAEL
DISTEFANO
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Goodearl, A.D.J., Glucksmann, A.M., Xie, M. and Distefano, Gpotearl Coupled receptor and utilization thereof Patent: JP 2001525174-A 1 11-DEC-2001;
MILLENNIUM PHARMACEUTICALS INC
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                           CAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTCGTCGGCGCCCTTCTGCATCCC
                                                         CTCGGCAGCCTGGACCGCGCTGCTGGCCGCGCTCATGGCGCTCATCGTGGCCACGGT
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              CAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTCGTCGGCGCCTTCTGCATCCC
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Strandedness: Single;
Topology: Linear;
G protein-coupled receptor and utilization thereof FH Key Location/Qualifiers
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1. .2689
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2665 ATTTTTTTAAAAAAAAAAAAAAA 2688 2656 ATTTTTTAAAAAAAAAAAAAA 2679	da Qy	.585 CCAGAAGCTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAGTG
2605 ATGCTCCTCTGCCTGTGCCCGCTGCGCTGCAAACCGTGAGGTCACAATAAAGTGT	D Qy	\$25 TGTCCTCTACCCTCTGTGCCACACACACTTCCGCCGGGCCTTCACCAAGCTGCTCTGCCC 1
2545 GGAGGTGCCCGGGCAGGGGCCGCTTCGCCATGTGCTGCACCCGTGCCACGCGCTCTGC	Qy Db	1465 CCCTGACTACTGGTACGAAACCTCCTTCTGGCTCCTGTGGGCCAACTCGGCTGTCAACCC 1524
485 G 476 G	D QY	1405 CTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCCGCCTGCCATGGCCACTGCGT 1464
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245 A 236 A	9 4g	1165 GACCCTCGGGGGTGGGGGTGGGGCTCCGTGGCTTCACCCACC
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825 C	д . Q	745 GCGGCGGGAAGATGCTGCTGGTGTGGGTGCTGGCTTCCTGCTGTACGGACC 804
765 A 757 A	, p 5	685 CTACGACCGCTTCCTGTCGGTCACCCGAGCGGTCTCATACCGGGCCCAGCAGGGTGACAC 744
97 Q—q	£ 5	625 GTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGCCTTCAACATCGTGCTCATCAG 684
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70 CATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCGAGCGGTCTCATACCGGGC 72	10 GGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGCCTTCAA	43 C-C	490 CCTCCGCACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTCGTCGG 549	430 CATCGTGGCCACGGTGCTGGGCAACGCGCTGGTCATGCTCGCCTTCGTGGCCGACTCGAG 489	70 63	310 GCCGCCGACGGGCCGTGAACGCTTCGGGGGGGGCGTGGCGGGGGATGCGGCGGCGGGGGGGG	250 CGGCCGGCGCCCCGCGTCCCGGAGCCGGGAGCCTGAGCCTGCGGGGCCATGGAGCGCGC 309	190 GGCCAAGGGCCCGCAAAGACGAGGCTCCCGGGCCGGGCC	130 CTGGCCCCGGCCCCGCGGACCATGCGCTGGGGGCCCCCAGGGGAAACCCGACCC 189	70 GCCGCGCTGCCGGCCCCACTGGGCTCGGATCCGGCCCCGGCCCCTCGGCACCGCCTGCT 129	ACCGGCAGCGGCTCAGGCTCCGCTCTCCCGCTCAGCTCCGCTCAGGCTCAGGCAGCGGCTCAGGCTCAGGCTCCGGCTCCTCTCCCGCTC	Query Match 97.5%; Score 2632; DB 6; Length 2665; Best Local Similarity 99.7%; Pred. No. 0; Matches 2657; Conservative 0; Mismatches 5; Indels 2; Gaps 2;		Patent: WO 02068579-A 16386 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof	Homo saplens Homo saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	0452 0452.1 GI:	CQ730452 2665 bp DNA linear PAT 03-FEB-2004 Sequence 16386 from Patent WO02068579.
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1750 TETEGECCETETTAATGCCACGGCAGCCACCCTGCCATGGAGGCGCCTTCCTGGGTTGG	1690 GCATCTGGCCCTGCTGCCCCTACCCGGCTTCCCCCAGGGGTGAGCCCCGCCGTGTC	1630 GAAGTGACTGGCCCACCAGAGCCTCCCTCAGCCACGCCTCTCTCAGCCCAGGTCTCCTGG	63	03	1450 CCATGGCCACTGCGTCCCTGACTACTGGTACGAAACCTCCTTCTGGCTCCTGTGGGCCAA	1390 GAGCATCTTTGGGCTCTGCTGGGCCCCCATACACGCTGCTGATGATCATCCGGGCCGCCTG	1330 CACCCAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCCAAGTCGCTGGCCGTCATCGT		203	150 143	1090 GGGCACGGGAAGGCCATGCCGCTGCACAGGTATGGGGTGAGTGA	1030 CCCTCCCGAGGCCCAGCCCTCACCACCCCCACCGCCTGGCTGG	970 CATCCAGAGGCGCACCCGCCTCCGGCTGGATGGGGCTCGAGAGGCAGCCGGCCCCGAGCC	910 CCTGGAGTTCTTTACGCCCTTCCTCAGCGTCACCTTCTTTAACCTCAGCATCTACCTGAA	850 CGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATCACGGCTTCCAC	790 CCTGCTGTACGGACCAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGCAGCTCCATCCC	730 CCAGCAGGGTGACACGCGGGGGGGCAGTGCGGAAGATGCTGCTGGTGTGGGTGCTGGCCTT	

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HS1005F21

100976 bp DNA linear PRI 24-APR-2001 Human DNA sequence from clone RP5-1005F21 on chromosome 20 Contains the PSMA7 gene for proteasome subunit 7, alpha type (prosome, macropain), the HRH3 gene encoding histamine receptor H3, the XIAA0693 gene similar to SSXT (synovial sarroma, translocated to X chromosome), a novel gene for a GTP-binding protein, the 3' end of a novel gene similar to Pleurodeles waltlii RAPP5 protein, 7 CpG islands, ESTs, STSs and GSSs, complete sequence.
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AUTHORS
TITLE
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ORGANISM
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On Jul 23, 2000 this sequence version replaced gi:8919366.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
This sequence is the entire insert of clone RP5-1005721 The true
left end of clone RP11-11720 is at 51899 in this sequence. This
sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
assembly was confirmed by restriction digest. RP5-1005721 is from
the library RPCI-5 constructed by the group of Pieter de Jong. For
further details see
http://bcrac/home.htm
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AL078633.32 GI:9408092
HTG; CpG island; GTP-binding protein; histamine receptor; HRH3;
KIAA0693; macropain; PMSA7; prosome; proteasome; SSXT; synovial
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Submitted (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 100976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
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/note="MER45 repeat: matches 1. .116 of
3564. .3753
                          /note="33 copies 2
5181. .5276
                                                                   /note="34 copies 2 5116. .5181
                                                                                                                                             /note="4 copies 14 mer
5041. .5110
                                                                                                                                                                                                                                           /note="10 copies 19 mer
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/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                      note="MLT1J repeat: matches 137. .370 of consensus"
                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 80. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP5-1005F21"
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1 6229. .6376
1 /note="4 copies 37 mer 69% conserved"
6333. .6652
1 /note="10 copies 32 mer 67%
6353. .6454
1 /note="10 copies 32 mer 67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="3 copies 82 mer 72% conserved"
5937. .6158
/note="6 copies 37 mer 72% conserved"
5943. .6176
/note="6 copies 39 mer 68% conserved"
6128. .6199
/note="3 copies 24 mer 84% conserved"
6130. .6199
/note="5 copies 14 mer 75% conserved"
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/note="7 copies 10 mer g

6425. . 6498

/note="37 copies 2 mer g

6480. . . 6631

/note="8 copies 19 mer 7
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/note="5 copies 34 mer 7

6852. .6903

/note="26 copies 2 mer c

6909. .6992
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/note="12 copies 14 mer 69% conserved"

5640. .5787

/note="4 copies 37 mer 77% conserved"
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'note="5 copies 39 mer 65% conserved"

5386. .5931

'note="76 copies 21 mer 54% conserved

5407. .5678
                                                                                                          /note="6 copies 14
5910. .6989
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note="4 copies 33 mer 72% conserved"

5760. .5825

note="33 copies 2 mer gt 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5002. 5669
5002. 5669
note="7 copies 24 mer 69% conserved"
5507. 5676
Foote="17 copies 10 mer gtgtgtgtgt 69:
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/note="201 copies 2
                    note="FLAM_C repeat: matches 1. .133 of consensus"
                                                    note="46 copies 2 mer gg 62% conserved"
                                                                                        note="40 copies
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te="11 copies 33
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1. .6176
te="3 copies 82 mer
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:e="12 copies 32
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                                                                                                                                                                                                                       CGGACCAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGCAGCTCCATCCCCGAGGGCCA
                                                                                                                                                                                                                                                                                                                                                 CTTCCGCCCCCCCCGACCAGCCTGCCCTTCTGCAGGTCTCATACCGGGCCCAGCAGGG
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                    GCGCACCCGCCTCCGGCTGGATGGGGCTCGAGAGGCAGCCGGCCCCGAGCCCCCTCCCGA 1038
                                                                            CTTTACGCCCTTCCTCAGCGTCACCTTCTTTAACCTCAGCATCTACCTGAACATCCAGAG
                                                                                                                             CTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATCACGGCTTCCACCCTGGAGTT
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Conservative
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Em:S76942 Em:AF108017 Em:S45235 Em:AF149717 Em:U07882
Em:AF246718 Em:U10504 Em:U86601 Em:AK023527 Em:AF162010
Em:AF162011 Em:U10504 Em:U3821 Em:AF012958 Em:U00475
Em:S56143 Em:L24445 Em:AB004662 Em:AF013958 Em:U00475
Em:AF176838 Em:U51098 Em:AF162009 Em:Y14493 Em:L22214
Em:U04279 Em:AF162008 Em:AF266468
Em:ED63702 Em:BF647364 Em:B00466 Em:AF7218 Em:BB783826
Em:BE063702 Em:BE647364 Em:H20846 Em:AF7218 Em:BB783826
Em:H28163 Em:BA943666 Em:P30372 Em:AH152091 Em:BB429590
Em:H28163 Em:BB43989°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="dJ1005F21.1 (histamine receptor H3 )"
/product="match: CDNAs: Em:AF140538 Em:AB01546 Em:AB019000
/prote="match: CDNAs: Em:X04413 Em:AF237919 Em:AF267537
Em:AF267538 Em:M22926 Em:X04413 Em:AF237919 Em:AF287537
Em:AF262626 Em:AF307973 Em:AB044934 Em:M32061 Em:AF188626
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'note="7 copies 14 mer 69% conserved"
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11214. .11309
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gene="HRH3"
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note="9 copies 10 mer ggggggcggg 67% conserved"
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3421. .20706
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.ote="14 copies 9 mer ggggggggc 61% conserved"
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|ote="CpG island"
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te="22 copies 2
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Pred. No. 4.3e-256;
0; Mismatches 21;
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                                               Koga,H.
Primers for synthesizing full length cDNA clones
Patent: EP 1396543-A 2796 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Sequence 2796 from Pater
CQ782656
CQ782656.1 GI:45502599
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1549 Qy 2570 CGCCATGTGCTC	9 Qy 2510 9 Db 1740	1429 Qy 2450 CCACTCTGTTTC	9 Qy 2390 Db 1620	9 Qy 2330 9 Db 1560	9 Qy 2270 9 Db 1500	9 Qy 2210 9 Db 1440	9 Qy 2150 9 Db 1380	QY 2090 TGCCTTTGCTGC	1260	0 0	1910	1081	1021	961	901	1670 841	1550 781	721
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830 TCCGGGGGCAGCTCCATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTAC 889	770 CTGGTGTGGGTGCTGGCCTTCCTGCTGTACGGACCAGCCATCCTGAGCTGGGAGTACCTG 829	710 CGAGCGGTCTCATACCGGGCCCAGCAGGGTGACACGCGGCGGCAGTGCGGAAGATGCTG 769	650 TGCACCTCCTCCACAACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACC 709		530 ATCTCCGACTTCCTCGTCGGCGCCTTCTGCATCCCACTGTATGTA	atch 60.6%; Score 1636.2; DB 6; Length 1902; al Similarity 88.6%; Pred. NO. 4.1e-213; 1899; Conservative 0; Mismatches 3; Indels 241; Gaps 2;	/ox /mo /db	Location/Qualifiers FT CDS (235). (864). Location/Qualifiers 1. 1902	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length CDNA and use thereof FH Key	PI TETSUJI OTSUKI,HISASHI KOGA PC	PI ISHII, PI YURI KAWAI,AI WAKAWATSU,TOMOYASU SUGIYAMA,KBIICHI NAGAI, PI	PF 07-2004 PF 07-2000 JP 2000253172 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO	OS Homo sapiens (human) PN 202017375-A/2679	Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2679 22-JAN-2002; HELLY RESEARCH INSTITUTE		-	BD127248 BD127248.1 GI:23222193 JP 2002017375-A/2679. Homo sapiens (human)	BD127248 1902 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof.		2630 GCTGCCCTGCAAACCGTGAGGTCACAATAAAGTGTATTTTTTT 2672
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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AK(074730.1 GI:22760362
Oligo capping; fis (full insert sequence)
Homo sapiens (human)
                                                              Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
                                                                                                                                                                                                                                                  AK074730 1902 bp mRNA linear Homo sapiens cDNA FLJ90249 fis, clone NT2RM2001941, to MUSCARINIC ACETYLCHOLINE RECEPTOR M1.
             Unpublished 2 (bases 1
2 (bases 1 to 1902)
Isogai, T. and Otsuki, T.
                                       Ninomiya, K.
NEDO human cDNA sequencing
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Catarrhini; Hominidae;
                                                                                                                                                       Hominidae;
                                                                                                                                                                                                                                                                 PRI 03-SEP-2002 weakly similar
                                                                                                                                                                    Euteleostomi;
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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human CDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology; cDNA full insert sequencing:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
GAGGCAGCCGGCCCGAGCCCCTCCCGAGGCCCAGCCCTCACCACCCCCACCCGCCTGGC
                                                                   AACCTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCCTCCGGCTGGATGGGGCTCGA
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235. .867
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_	2150 CCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGGCCCTAGGAACCTCGAAGCTGTTCT 2209	Ş
FEATURES Description of the source of the so	1320 TGCCTTTGCTGCCTTCTGTCTCTTGCATAAGCCTCAGGCCTTGGCCCTTTCACCCCTCTTC 1379	В
FH Key FT exon	2090 IGCCTTIGCTGCCTTCTGCTTGCATAAGCCTCAGGCCTGGCCCTTTCACCCCTCTTC 2149	ફ
C12N5/10, PC C12P2	2030 ACCTGCACACCCCTGCACACACCTGCACACCGTCCCTCTCCCCGGACAAGCCCAGGACAC 2089	B &
PI KENIC PI KENIC PI YUSUK PC C12N1	1970 CAAGCACCTGGGTGTGCTCCAGGCTTCCTGCCCTAGCAGTTTGCCTCTGCACGTGCACAC 2029	D Q
	1910 GCTGCCCACCCCTGCTGGTGCCCACCCTTCGCAGTTACTGGTTGTTCCTTCC	B 8
receptor p JOURNAL Patenic p BANYU PHAP COMMENT OS Homo	1850 CGGCCTGCCCCCACATTCTGGCTCCACCGGGAGGACAGTCTGGAGGTCCCAGACAT 1909	B 8
REFERENCE 1 (bases AUTHORS Itaya,K., Hidaka,K., TITLE Novel quan	1790 GAGGCGCCTTCCTGGGTTGGCCAGAGGGCCCCTCACTGGCTGG	B 8
SOURCE Homo sapie ORGANISM Homo sapie Eukaryota; Mammalia;	1730 GGGGTGAGCCCCGCGTGTCTGTGGCCCTCTTTAATGCCACGGCAGCCACCCTGCCATG 1789	B 8
	1670 TCTCAGCCCAGGTCTCCTGGGCATCTGGCCCTGCTGCCCCCTACCCGGCTCGTTCCCCCA 1729	<u> </u>
RESULT 13 E39817 LOCUS E39817 DEFINITION Novel quan	1610 AGCTCCCTGGAGCACTGCTGGAAGTGAGTGGCCCACCAGAGCCTCCCTC	p
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1740	1430 ATGATCATCCGGGCCGCCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGAAACCTCC 1489	B 8
	1370 AAGTCGCTGGCCGTCATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCATACACGCTGCTG 1429	B 8
Db 1620 CTGCTTCTG	1310 AAGATGGTGTCCCAGAGCTTCACCCAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCC 1369	Db Qq
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Qy 2270 ATGITCGT	GGCTCCGTGGCTTCACCCACCTCCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGGCCG	8
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)EC-1998 WO PCTJP9805967
ITAYA, TETSUO TAKIMURA, TAKAO NAKAMURA, MASAHIKO KOBAYASHI,
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Takimura, T., Nakamura, T., Kobayashi, M., Tana, K.,
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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Itadani,H., Takimura,T., Nakamura,T.,
Hidaka,Y. and Ohta,M.
Guanosine triphosphate (GTP) binding property
                                                                                                                                                                          Unclassified.
                                                                                                                                                                                                                                                                                                         CAAAATTGCTGAGGAGCTC
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/mol_type="genomic
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Yao, B.B., Sharma, R., Cassar, S., Esbenshade, T.A. and Cloning and Pharmacological Characterization of the Histamine H3 Receptor
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AY231164 1
Macaca mulatta histamine
AY231164
AY231164.1 GI:29124990
                                                                                                                                                                   Submitted (07-FEB-2003) R-4MN, Abbott Park Road, Abbott Park, Location/Qualifiers
                                                                                                                                                                                                                   Cassar, S., Esbenshade, T.A., Hancock, A.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Crániata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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/mol type="mRNA"
/db xref="taxon:9544"
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/gene="HRH3"
/note="G protein-coupled receptor"
/codon_start=1
                                                     /gene="HRH3"
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Search completed: Job time: 11703.2 2 2005, 10:53:01

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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11091.610 Million cell updates/sec
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Aac62365 Complete
Abn84882 Human his
Abz42533 Human his
Acc59394 Human his
Acc59394 Human nis
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Add2880 Human mor
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Ad310763 Full leng
Aax84882 G-protein
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Aa159976 Human wil
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Rat G pro
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1072.2	1075.2	1082.6	1156	1178.6	1201.8	1204.8	1207.8	1208	1272.6	1303.8	1330.8	13	1335			1335			1348.4		1360		1384.8	1384.8
39.7	39.8	40.1	42.8	43.7	44.5	44.6	44.7	44.8	47.2	48.3	49.3	49.3	49.5	49.5	49.5	49.5	49.5	49.5	50.0	50.3	50.4	50.4	51.3	51.3
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Aah44575 Rat musca	Abz82337 Mouse his	Aal59985 Human H3	Aas76868 DNA encod			Aax84571 G-protein				Aa159978 Human H3	Human	Aax02886 Human mAC	Adr31457 Human his					Ado29966 Human GPC			-	Aax84572 Human G-p	Abx11853 Rat cDNA	Aah44574 Rat musca

ALIGNMENTS

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P-PSDB; AAY92218.
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The cDNA encodes the human histamine H3 receptor. The polypeptide contains the seven conserved hydrophoral comains and specific residues conserved in biogenic amine receptors. The human histamine H3 receptor polynucleotides and polypeptides are used in methods to screen for

Claim 2; Fig 1A-B; 54pp; English.

Novel human histamine H3 receptor polynucleotides and polypeptides used in methods to identify modulators of receptor activity.

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0	\$ B \$ 8	P & B &	Qy db	P 6	B 8	B 8	B 성	B &	B 8	B 8	D Q	B 8	당 \$	a a
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                                  TGCCTTCAACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCGAGCGGTCTC
                                                                                                                                                                                                                 CGACTCGAGCCTCCGCACCCAGAACACTTCTTCCTGCTCAACCTCGCCATCTCCGACTT
                                                                                                                                                                                                                                    CGACTOGAGCCTCCGCACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTT
                                                                                   CTTCGGCCGGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGCACCTCCTC
                                                                                                 CTTCGGCCGGGGCCTCTGCAAGCTGTGGCTGGGTAGTGGACTACCTGCTGTGCACCTCCTC
                                                                                                                                                  CCTCGTCGGCGCCTTCTGCATCCCACTGTATGTACCCTACGTGCTGACAGGCCGCTGGAC
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WPI; 2001-023168/03

Novel DNA molecules useful in gene therapy for the treatment inflammation or allergy, or for encoding a human histamine H3 and identifying histamine receptor modulators that are useful therapeutic and diagnostic agents. receptor

The present sequence represents the complete sequence of cDNA encoding a human histamine H3 receptor. The histamine H3 receptor DNA molecules are useful for isolating homologues of receptor, identifying and isolating genomic equivalents of receptor, and identifying, detecting or isolating mutant forms of the receptor. The DNA molecules are also useful in gene therapy for the treatment of inflammation or allergies. The human histamine H3 receptor protein is useful in identifying modulators of the human histamine H3 receptor, which in turn are useful as therapeutic and the standard of the human histamine H3 receptor, which in turn are useful as therapeutic and the standard of the human histamine H3 receptor, which in turn are useful as therapeutic and the standard of the st

C; 805 G; 502 T; 0 U; 0 Other;

CCGCCTGCTCTGGCCCCGGGCCCCGGGCCCCGCGGACCATGCGGTGGGGGCCCCCCAGGGGAA 180 GCTGCAGCAGCCGCGCTCCCCCCACTGGGCTCGGATCCGGGCCCCCGGGCCCCCTCGGCA CCACGCGTCCGCCGGCTGCACGGTCGCACCGGCAGCGGCTCAGGCTCCCGGCTCCTCTCCC GCCCTCCTCATCCTGCCCACGCTGCTGCCGCAACGCCCTTGCTCGCCTTCGTGGC CCCAGCTCTCGGCCGGCGCCCTGCCCCGCGTCCCGGAGCCGGCGTGAGCCTGCGGGGCCAT ACCCGACCCGGCCAAGGGCCCGCAAAGACGACGACCTCCCGGGCCGGGCCCCTCCCCGGCCG CCGCCTGCTCTGGCCCCGGCCCCGGCCCGGCCGACCATGCGCTGGGCGCCCCCCAGGGGAA CCACGCGTCCGCCGGCTGCACGGTCGCACCGGCTCAGGCTCCGGCTCCTCTCCC GGCGGCGGGGGGCGCGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCCGCGCTCAT CCCAGCTCTCGGCCGGCGCCTGCCCCGCGTCCCGGAGCCGTGAGCCTGCGGGGCCAT ACCCGACCCGGCCAAGGGCCCGCAAAGACGAGGCTCCCGGGCCGGGCCCCTCCCGGCCG Score 2699; Pred. No. 0; 0; Mismatches B <u>,</u> 4. Length Indels ٥. Gaps 420 300 120 120 480 480 420 360 360 300 240 240 180 60

720

1860	1801 CTGGGTTGGCCAGAGGGCCCCTCACTGGCTGGACTGGAGGCTGGGTGGCCGGCC
80	741 CGCCGTGTCTGTGGCCCTCTTAATGCCACGGCAGCCACCCTGCCATGGAGGCGCCCTTC
1800	.741 CGCCGTGTCTGTGGCCCTCTTAATGCCACGGCAGCCACCCTGCCATGGAGGCGCCTTC
1740	1681 GTCTCTGGGCATCTGCTCCTCCTCCCGCTCGTTCCCCCAGGGTGAGGGTGAGCCC
68	621 GCACTGCTGGAAGTGAGTCGCCCACCACACCCTCTCTCTC
1680	621 GCACTGCTGGAAGTGAGTGGCCCACCAGAGCCTCCCTCAGCCACGCCTCTCTCAGCCCAG
1620 1620	1561 GGCCTTCACCAAGCTGCTCTGCCCCCAGAAGCTCAAAATCCAGCCCCACAGCTCCCTGGA
1560 1560	SO1 GTGGGCCAACTCGGCTGTCAACCCTGTCCTCTACCCTCTGTGCCACCACAGCTTCCGCCG
1500	441 GGCCGCCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGAAAACCTCCTTCTGGCTCCT
1500	441 GGCGGCCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGAAACCTCCTTCTGGCTCCT
1440 1440	381 CGTCATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCG
1380 1380	321 CCAGAGCTTCACCCAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCCAAGTCGCTGGC
32	261 GAGGGGTTCCAAGCCGTCGGCGTCGCTCGCTGGAGAAGCGCATGAAGATGGTGTC
32	261 GAGGGGCTCCAAGCCGTCGGCGTCCTCGGCCTCGCTGGAGAAGCGCATGAAGATGGTGTC
1260 1260	1201 TTCACCCACCTCCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGGCCGCGCTCACTCA
1200	141 CGTAGGCGCTGAGGCCGGGGAGGCGACCCTCGGGGGTGGCGGTGGGGGCGGCTCCGTGGC
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1080	3AGCCCCTCCCGAGGCCCAGCCCTCACCACCCCCCCCCCC
8	.021 CCCCGAGCCCCCCCCGAGGCCCAGGCCTCACCACCGCCACCGCCTGGCTGG
1020	961 CTACCTGAACATCCAGAGGCGCACCCGCCTCCGGCTGGATGGGGCTCGAGAGGCAGCCGG
960	901 GGCTTCCACCCTGGAGTTCTTTACGCCCTTCCTCAGCGTCACCTTCTTTAACCTCAGCAT
900	841 CTCCATCCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATCAC
840 840	781 GCTGGCCTTCCTGCTGTACGGACCAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGCAG
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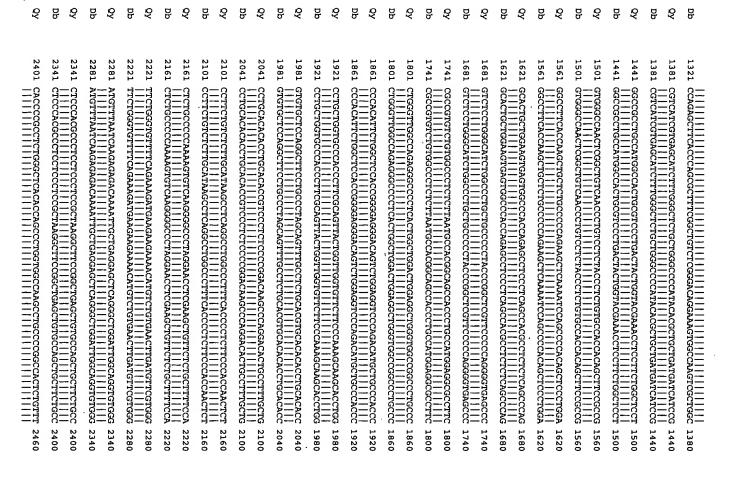
RESULT 3
ABN84882
ID ABN84882 standard; cDNA; 2699 BP.

XX
AC ABN84882;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human histamine H3 receptor cDNA.
XX
KW Histamine; receptor; G-protein coupl
KW cardiant; antidepressant; tranquilli
KW hypotensive; analgesic; antidiabetic Histamine; receptor; G-protein coupled receptor; human; neuroprotective; cardiant; antidepressant; tranquillizer; antiparkinosinian; anorectic; hypotensive; analgesic; antidiabetic; laxative; antiarrythmic; antiulcer;

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CC histamine H3 receptor, a novel G-protein coupled receptor. The Clone was C isolated from a human thalamus CDNA library using a histamine H3 receptor CC probe. Histamine H3 receptor CDNA has been expressed in recombinant host C cells, which produced active recombinant protein. H3 receptor uccleic cells, which produced active recombinant protein. H3 receptor nucleic CC acids and proteins can be used to identify modulators of H3 receptor CC central nervous system disorders, such as depression, anxiety, psychoses (e.g. schizophrenia), tardive dyskinesia, Parkinson's disease, obesity, CC hypertension, Tourette's syndrome, sexual dysfunction, drug addiction, CC drug abuse, cognitive disorders, Alzheimer's disease, senile dementia, CC obsessive-compulsive behaviour, panic attacks, pain, social phobias, CC eating disorders and anorexia, cardiovascular and cerebrovascular CC disorders, non-insulin dependent diabetes mellitus, hyperglycaemia, CC constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity, as well as acid secretion, ulcers, airway constriction, CC asthma, allergy, inflammation and prostate dysfunction. Histamine H3 CC receptor DNA molecules are also useful for isolating related sequences, CC identifying and isolating genomic equivalents, identifying, detecting or isolating mutant forms of DNA, and in gene therapy
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Matches 2699
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P-PSDB; ABB79792.
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tive 0; Mismatches
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RRSULT 4
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ARZ Human 04-MAR-2003 histamine H3 receptor (first entry) nucleotide SEQ Ħ

NO:548

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; g protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; gene; dg.

Homo sapiens.

WO200261087-A2

08-AUG-2002

19-DEC-2001; 2001WO-US050107.

19-DEC-2000; 2000US-0257144P.

(LIFE-) LIFESPAN BIOSCIENCES INC.

Burmer , მ Roush Ę, Brown

JP;

2003-046718/04 ABP81687

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating condit: in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer o diseases. conditions

Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific

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Best Local Similarity
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Human; histamine H3 receptor; receptor modulator; gene; ds; agonist; nootropic; neuroprotective; cerebroprotective; cardiant; antiasthmatic; immunomodulator; gastrointestinal; antiallergic; antidiabetic; antiinflammatory; hypotensive; antiarrhythmic.
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Best Local Similarity
Matches 2699; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying agonists of recombinant human histamine H3 receptor protein activity, useful for diagnosing and treating H3 receptor-related disorders, such as nervous system disorders, asthma, allergy, hypertension and diabetes.
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                                                                          activity of the human histamine H3 receptor in response to ligand binding. The antibody is useful for detecting and quantifying expression of human histamine H3 receptors, which may be useful for diagnostic, epidemiological or forensic purposes. The antibody is potentially useful in treating diseases such as depression, anxiety, schizophrenia, parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual dysfunction, drug addiction or drug abuse, cognitive disorders, historders disease, obsessive-compulsive behaviour, panic attacks, pain, eating disorders and anorexia, cardiovascular and cerebrovascular disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy, inflammation, or prostate dysfunction. The present sequence is the full
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a monospecific antibody immunologically reactive with a protein appearing as ADD22854, where the protein functions as a human histamine H3 receptor. The antibody blocks intracellular signaling
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                CCTGCACACACCTGCACACCGTCCCTCTCCCCGGACAAGCCCAGGACACTGCCTTTGCTG
                                     GTGTGCTCCAGGCTTCCTGCCCTAGCAGTTTGCCTCTGCACGTGCACACACCCTGCACACC
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08-MAY-2003; 2003US-0468775P.
19-MAY-2003; 2003US-047814P.
16-JUN-2003; 2003US-0478742P.
18-JUL-2003; 2003US-0478742P.
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ID ADG89179 standard; cDNA; 2699 BP.

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DT 21-OCT-2004 (first entry)

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DE Human urological disorder related protein 8203 encoding cDNA SEQ:131.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a human histamine H3 receptor protein and nucleic acid encoding such protein. The invention is useful for identifying compounds that modulate the activity of human histamine H3 receptor. The invention is useful for treating a condition that is mediated by a human histamine H3 receptor in a patient and for treating Parkinson's disease, obesity, Alzheimer's disease, pain, stress, ulcers, constipation and non-insulin dependent diabetes mediates. The present sequence is a human histamine H3 receptor cDNA.
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(ERLA/) ERLANDER M.
(HUVA/) HUVAR A.
(PYAT/) PYATI J.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated and purified human histamine H3 receptor protein useful for identifying modulators utilized for treating Parkinson's disease, obesity, Alzheimer's disease, pain, stress or ulcers.
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P-PSDB; ADR31458.
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21-AUG-2000; 2000US-00642852.
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                                                                                                             GCTGCAGCAGCCGCGCTCCCGGGCCCCACTGGGCTCGGATCCGGCCCCCGGCCCCCTCGGCA
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This invention describes the isolation of a novel human muscarinic acetylcholine receptor 6 (mACHR-6), capable of modulating the effect acetylcholine on acetylcholine responsive cells. mACHR-6 cDNAs and polypeptides may be used to detect naturally occurring mutations of mACHR-6 gene and determine if a subject with the mutated gene is at
                                                                                                                                                                                                                                         Nucleic acids encoding modulating the effects
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cc of (or is predisposed to have) a mACHR-6 related disorder, modulate cell activity mediated by mACHR-6 (e.g. biological processes mediated by phosphatidylinositol turn-over and signalling), secretion of a molecule (e.g. a neurotransmitter or a glandular enzyme), or contraction of a contraction of a smooth muscle cell, treat disorders mediated by abnormal mACHR-6 activity (e.g. prevous system disorders (e.g. amnesia, apraxia, agnosia, amnestic dysnomia, amnestic spatial disorientation, Kluver-Bucy syndrome, contraction of a contraction contraction contraction contractions, perceptual disorders mediated by abnormal agnosia, amnestic contractions, perceptual disorders, and learning disability, visual contractions, perceptual disturbances, and Lewry body dementia contractive despression contractives, and body temperature of preparative disorders (e.g. sleep-wakefulness, and body temperature or repiratory depression contractives (e.g. related to irritable bowel syndrome (188), or chest pain), movement contractive contractive disorders (e.g. related to parkinson's disease), eating disorders (e.g. contractive alivary disease), cardiac disorders (e.g. flashetic polydipsia), smooth muscle related disorders (e.g. 188, contractive alivary disease), cardiac disorders (e.g. pathologic chronic obstructive alivary disease), cardiac disorders (e.g. pathologic chronic contractive alivary disease), cardiac disorders (e.g. pathologic chronic contraction (e.g. xerostomia and diabetes mellitus)
    Sequence
    2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;
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Similarity

Score Pred.

No. 0;

DΒ

2;

Length

S 밁 S ફ 밁 δ ð 밁 Ś 밁 S 밁 Ś 밁 Ś 밁 ঠ В 밁 밁 Ś Query Match Best Local S Matches 2659; 505 437 377 317 557 497 445 385 325 257 265 197 205 138 145 78 85 18 25 GTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGCCTTCAACATCGTGCTCATCAG CAACTICTTCCTGCICAACCICGCCAICTCCGACTTCCTCGGCGGCGCCTTCTGCATCCC GCCCCGCGGACCATGCGCTGGGCGCCCCCAGGGGAAAACCCCGACCCGGCCAAGGGCCCGCA CGCACCGGCAGCGGCTCAGGCTCCGGCTCTCCCCGCTGCAGCAGCCGCGCTGCCGGCC ACTGTATGTACCCTACGTGCTGACAGGCCGCTGGACCTTCGGCCGGGGGCCTCTGCAAGCT GCTGGGCAACGCGCTGGTCATGCTCGCCTTCGTGGCCGACTCGAGCCTCCGCACCCAGAA CTCGGCAGCCTGGACCGCGGTGCTGGCCGCGCTCATGGCGCTCATCGTGGCCACGGT CTCGGCAGCCTGGACCGCGGTGCTGGCCGCGCCTCATGGCGCTGCTCATCGTGGCCACGGT CGCACCGGCAGCGCTCAGGCTCCGGCTCCTCTCCCGCTGCAGCAGCCGCGCTGCCGGCC ACTGTATGTACCCTACGTGCTGAC CAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTCGTCGGCGCCCTTCTGCATCCC GCTGGGCAACGCGCTGGTCATGCTCGCCTTCGTGGCCGACTCGAGCCTCCGCACCCAGAA Conservative 97.6%; 0, Mismatches ű Indels 2; Gaps 684 616 624 556 564 496 504 436 444 376 384 316 324 256 264 196 204 137 144 77

1645 CCAGAGCCTCCCTCAGCCACGCCTCTCAGCCCAGGTCTCCTGGGCATCTGGGCCTGCT 1704	### CONTROLL CONTROL CON
RESULT 10 AAX59167 ID AAX59167 standard; cDNA; 2689 BP. XX AC AAX59167; XX DT 06-SEP-1999 (first entry) XX DE Human G protein coupled receptor flh84g5 cDNA.	Db 1757

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This nucleotide sequence, the coding region of which is claimed, codes for a novel human 6 protein coupled receptor, termed filh495 (see CR ANY05122). The filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 polymucleotides of filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 polymucleotides of filh495 fragment (see also ANX59168) as probe. The clibrary using a rat filh495 polympetides and antibodies; and a method of cmodulating polymucleotide channel, expression vectors, host call; interact with a filh495 polympetides and antibodies; and a method of cmodulating polympetide channel or a potassium or calcium channel; (iv) modulate with a grotesion or another protein which naturally binds continued to filh495 polympetides; and a method of carnitine from a few continued continued to the continued to filh495 polympetide activities of a neuror ransmitter; e.g. acetylcholine or carnitine from a neuror ransmitter; e.g. acetylcholine or carnitine from a few continued to filh495 polympetide activity such as a revous system related disorders, e.g. ammesta, apraxia, agnosia, and continuences are cativity. The products can be used to treat: disorders mediated by abnormal filh495 polympetide activity such as nervous system related memory loss and learning disability; disorders affective disorders such as visual hallucinations, perceptual continuences or delerium associated with Lewy body dementia, schitzo-fifted products of percession, paradoxical shown selective disorders such as REM sleep; disorders affecting pain generation mechanisms e.g. pain related to irritable bowel syndrome, and selecting pain percention related continuence, oceophageal achalasia or chronic obstructive carbyca
           G protein coupled receptor; flh84g5; human; diagnosis; screening; therapy; antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidepressant; antiarrythmic; antidiabetic; antiinflammatory;
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Human; muscarinic acetylcholine receptor 6; mACHR-6; detection; antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidiabetic; antidepressant; antiarrhythmic; antiinflammatory; carnitine; pain; G-protein coupled receptor; nervous system related disorder; xerostomia; disorders affecting consciousness; affective disorder; movement disorder; irritable bowel syndrome; drinking disorder; gland related disorder; smooth muscle related disorder; cardiac muscle disorder; eating disorder; diabetes mellitus; diagnosis; drug screening; ss.

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                          'product= "muscarinic
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(mACHR-6), which is a member of the G family of proteins. mACHR-6 has
antiparkinsonian, nootropic, neuroprotective. neuroleptic, antidiabetic
antidepressant, antiarrhythmic and antiinflammatory activities. The mACHR
c antidepressant is capable of modulating the effects of a G-protein coupled
receptor (GPCN) ligand such as acetylcholine or an acetylcholine like
c molecule such as carnitine, e.g. by modulating phospholipase C
signalling/activity. Products from the present invention can be used for
treating disorders mediated by abnormal mACHR-6 protein activity such as
nervous system related disorders, disorders affecting consciousness,
affective disorders such as REM sleep abnormalities, disorders affecting
c pain generation mechanisms such as pain related to irritable bowel.
Syndrome or chest pain, movement disorders, eating disorders, drinking
disorders, smooth muscle related disorders, cardiac muscle disorders, and
gland related disorders such as xerostromia or diabetes mellitus. The
products can also be used for detection, diagnosis and drug screening.
(Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                       nucleic acid encoding an isolated G-protein coupled receptor useful treating nervous system related disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2635.2; DB 2; Length 2689;
Pred. No. 0;
0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           Claim 3; Fig 1; 64pp; English
                                97US-00985090.
98US-00042780.
98US-00165543
                                                                                    (MILL-) MILLENNIUM PHARM INC
                                                                                                                    Glucksmann MA, Goodearl ADJ
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Best Local Similarity 99.8%;
Matches 2659; Conservative (
                                                                                                                                                      1999-394858/33.
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1817 CTGGCTGGACTGGAGGCTGGCTGGCCCTGCCCCCCACATTCTGGCTCCACC-GGGA
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Human; ss; gene; mACHR-6; muscarinic acetylcholine receptor-6; cognitive disorder; amnesia; amnestic spatial disorientation; Kluver-Bucy syndrome; Alzheimer's related memory loss; learning disability; consciousness disorder; visual hallucination; delirium; schizo-effective disorder; schizophrenia; depression; affective disorder; sleep disorders; pain generation disorder; irritable bowel syndrome; chest pain; movement disorder; parkinson's disease; eating disorder; insulin hypersecretion obesity; heart muscle disorder; bradycardia; tachycardia; arrhythmia; flutter; fibrillation; gland related disorder; xerostomia; diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding muscarinic acetylcholine receptor 6, mACHR-6.
2656 ATTTTTTAAAAAAAAAAAAAA 2679
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Location/Qualifiers 291. .1628 /*tag= a /product= "mACHR-6" Homo sapiens

US2002166131-A1. 07-NOV-2002

97US-00985090. 98US-00042780. 99US-00349755 08-JUL-1999; 04-DEC-1997; 17-MAR-1998;

Goodearl ADJ, Glucksmann MA;

WPI; 2003-298709/29. P-PSDB; ABG76405 New muscarinic acetylcholine receptor 6 (mACHR-6) nucleic acids and proteins, useful for modulating acetylcholine or phosphatidylinositol, particularly for treating e.g. schizophrenia, chest pain, tachycardia or arrhythmia.

Claim 7; Fig 1; 66pp; English.

The invention relates to an isolated human or rat muscarinic acetylcholine receptor 6 (mACHR-6) nucleic acid molecule and the encoded protein. Also included are (non-human) host cells comprising the mACHR-6 nucleic acid molecule, an antibody that selectively bind the polypeptide above, a method for producing the polypeptide by culturing the host cells cuch that the mACHR-6 nucleic acid is expressed, a method for detecting the presence of the mACHR-6 nucleic acid is expressed, a method for detecting the presence of the mACHR-6 polypeptide and nucleic acid, a method for identifying a compound that binds to the mACHR-6 polypeptide and a method for polynucleotide, polypeptide, antibody or modulator are useful in drug screening, pharmacogenetic assays for identifying diseases, allelic screening, pharmacogenetic testing, methods of treatment, plantanes or minitoring the effects during clinical trials. In particular, the mACHR-6 polynucleotide, polypeptide or antibody is useful for treating or disagnosing cognitive disorders (e.g. amnesia, amnestic spatial disorientations, Kluver-Bucy syndrome, Alzheimer's related memory loss or learning disability), disorders affecting consciousness (e.g. schizophrenia or depression), affective disorders (e.g. sleep disorders),

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disorders affecting pain generation mechanisms (e.g. pain related to irritable bowel syndrome, or chest pain), movement disorders (e.g. Parkinson's disease), eating disorders (e.g. insulin hypersecretion obesity), heart muscle related disorders (e.g. bradycardia, tachycardia, arrhythmia, flutter or fibrillation), or gland related disorder (e.g. xerostomia or diabetes mellitus). The present sequence encodes human mACHR-6
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase Chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites supplied and polynucleotide sequences have applications in diagnostics, for genefic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this called not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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Claim 1; SEQ ID NO 12671; 103pp; English.
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                                                                                              Human secreted protein; hyperproliferative disorder; autoimmune disorder; fimmune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.
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                                                                                                                                                                                                                                                                                                                                                                         Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH,
Gulukota K, Graham JR;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length cDnes were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                              their use
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K, Kojin
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Wakamatsu A, Sugiyama T, Nagai
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Database

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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
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0; Mismatches 9; Indels 3;
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/mol type="mkNA"
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/clone=!MacBc:5802702"
/lab host="numbolastoma, cell line"
/lab host="numbolastoma; cell line"
/clone lib="hull MGC_47"
/clone lib="hull MGC_47"
/note="Organ: brain; Vector: poTB7; Site 1: Xho1; Site_2:
BcoR1; cDN made by oligo-dT priming. Directionally
cloned into EcoR1/Xho1 sites using the following 5:
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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AGENCOURT_6740127 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802702
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     TCCCCCAGGGGTGAGCCCCGCCGTGTCTGTGGCCCTCTTTAATGCCACGGCAGCCACCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lettp://image.llnl.gov
http://image.llnl.gov
Plate: LiAMA1213 row: p column: 03
High quality sequence stop: 654.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MAGE:5732110"
/tissue_type="hippocampus"
/tissue_type="hippocampus"
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/clone=lib="NIH MGC_124"
/clone=lib="NIH MGC_124"
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Pred. No. 6.9e-131;
0; Mismatches 38;
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2020 ACGIGCACACACCIGCACACCCCIGCACACACACGCACACCGICCCICICCCC 2072

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651
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11920 row: m column: 07
High quality Sequence stop: 811.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 890)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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03354331F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5361966 5',
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/clone lib="NNH MGC 94"
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Site_2: SAL1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
                                                                    370 CACCTCCTCTGCCTTCAACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCG
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/db_xref="taxon:10090"
/clone="IMAGE:5361966"
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BI731453.1 GI:15708466
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AUTHORS
TITLE
JOURNAL
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E 1 (Dasses 1 to 732)

S NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: IRBIO2 row: b column: 06

High quality sequence stops: 610.
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/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-emplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-ECORV-XmnI/KhoI-3', 5'-ECORV-XmnI/KhoI-3', 5'-ECORV-XmnI/KhoI-3', 5'-ECORV-XmnI/KhoI-3', please visit our anonymous ftp site at please visit our anonymous ftp site at ftp://image.lnhi.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NHH_MGC Library."
                                                                                                                                                                                       CF147822
AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone
AMAGE:6971899 5', mRNA sequence.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                   CF147822.1 GI:33244090
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242 CCAGCTCTCGGCCGGCGCCCTGCCCGGGTGCGCGCGTGAGCCTGCGGGGCCTG 301
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                                                                                                                                                                                 20.1%; Score 543; DB 6;
88.1%; Pred. No. 3.4e-98;
iive 0; Mismatches 80
           Amgen EST Program.
Amgen Rat Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen. Inc
One Amgen Center Drive, Thousand Oa.
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
Location/Qualifiers
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Matches 591; Conservative
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AMGNNUC:URGP1-00001-D6-A urgpl (14349) Rattus norvegicus CDNA clone urgpl-00001-d6 5', mRNA sequence.
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                  CGTCAGCATCTACCTGAACATCCAGAGGGGCACTCGTCTTCGGCTGGATGGGGGCCGAAA
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                                                                                                                                                                                C-TCAGCATCTACCTGAACATCCAGAGGCGCACCCGCCTCCGGCTGGGATGGGGCTCGAGA
                                                                                                                                                                                                                                           GGCAGCCGGCCCCGAGCCCCCTCCCGAGGCCCTCACCACCCCCCCA----CCGCCTGG
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                                                                                                                                                   CTCATCACGCCTCCACCCTCGAGTTCTTCACACCCTTCCTCAGCGTTACCTTCTTCAAC
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6
                                                             890;
                                                          Score 549.6; DB 4; Length
Pred. No. 1.7e-99;
0; Mismatches 109; Indels
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Matches 663; Conservative
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SOURCE
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Gaps

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Length 672; 80; Indels 61

361 181 241 481 541

601 421 661 481 541

781 601

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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
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                                              1656 CTCAGCCACGCCTCTCTCAGCCCAGGTCTCCTGGGCATCTGGCCCTGCTGCCCCCTACCC 1715
                                                                                                                                                                                                                                                                                                                                              GCCTCGTTCCCCCAGGGGTGAGCCCCGCGGTGTCTGTGGCCCTCTTTAATGCCACGGCA 1775
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//clone_ligo dT_primed, full-length enriched cDNA library
//com_undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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181 AAATCCAGCCCCACAGGCTCCCTGGAGCACTGGTGGAAGTGGGCCCACCAGAGCCTCC 240
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1 (Dases 1 to 716)

Brandenberger, R., Rei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Lebkowski, J and Stanton, L.W.

Control human Es cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                        241 CTCAGCCACGCCTCTCTCAGCCCAGGCTCTCCTGGGCATCTGGCCCTGCTGCCCCTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 CGGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGCCCTTC
                                                                                                                                                                                                                                                                                              548 GGGGCCTTCTGCATCCCACTGTATGTACCCTACGTGCTGACAGGCCGCTGGACCTTCGGC
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17000424504731 GRN_ES Homo sapiens cDNA 5', mRNA seguence.
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100.0%; Pred. No. 8.8e-93;
iive 0; Mismatches 0;
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/lab host="Top10F" |
/clone_lib="BZN807043" |
/clone_lib="BZN807043" |
/clone_lib="BZN807043" |
/clone_lib="BZN807043" |
/clone_lib="BZN807043" |
/clone_lib="Grgan: Brain; Vector: pCNS-D2; Site_l: EcoRI;
Site_2: Not!; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The cDNA vector was adjusted to have about 6nnt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Osayama-Berg method. The
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 513)
Kim, N. S., Hahn, Y.; Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obtained cDNA vectors were used for transformation of competent cells E. coli Toplor by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kim YS
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 522; DB 6; Length 533; 99.8%; Pred. No. 5.4e-94; Cive 0; Mismatches 0; Indels
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Unpublished (2002)
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/db_xref="taxon:9606"
/clone="B2N807043-31-C05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: yongsung@mail.kribb.re.kr
Plate: 31 row: C column: 05
High quality sequence stop: 533.
Location/Qualifiers
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CB154982.1 GI:28140085
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I (bases I to 46)

Brandenberger, R., G., H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptome Characterization elucidates signaling networks that control human Es cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Regenerative Medicine

Geron Corporation
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/mol_trype="mrNA"
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/clone="IMAGE:3874260"
/tissue_trype="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Fechnologies."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
lt.G.E.Consortium/LLNL at:
lt.M.S.G.E.Consortium/LLNL at:
lt.M.S.G.E.Consort
                                                                                                                                                                                  GCCCAGCAGGTGACACGCGGGGGGGGGGAAGATGCTGCTGGTGGTGCTGCTGGCC
                                                                                                                                                                                                                                    TTCCTGCTGTACGGACCAGCCATCCTGAGCTGGGGAGTACCTGTCCGGGGGGCAGCTCCATC
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/organism="Homo sapiens"
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TITLE
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BE783826
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17.7%; Score 476.6; DB 2; Length 910;

Query Match

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217 ACCGGGCTGGGCGAAGAGCCGGCAAAGATTAGGCTCACGAGCGGGGCCCCACCCGGCCA 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 GGGGTGCTCATCGTGGCCACAGTACTGGGCAACGCGCTGGTCATGCTCGCCTTCGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.9%; Score 429.6; DB 7; Length 842; 83.7%; Pred. No. 1.9e-75; ive 0; Mismatches 90; Indels 15
                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol Lype="mRNN"
/db xref="taxon:10116"
/clone="IMAGE:7315203"
                                                                                                                                                                                                                                                                                                                                                                    sex="both"
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                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
                                                                                                                                                                                                                                                                                                                                                                                                          1652
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                                                                                                                                                                                                                  /clone lib="GRN ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 27526928 NIH MGC 254 Rattus norvegicus cDNA clone
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                                                                                                                                                                                                                                                                                                                                  Length 466;
230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658
Fai: 650 473 7760
Email: rbrandenberger@geron.com
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                              16.9%; Score 455; DB 7; 99.8%; Pred. No. 1.4e-80; ative 0; Mismatches 0;
                                                       Email: rbrandenberger@geron.com
Insert Length: 466 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Daniela S. Gerhard, Ph.D.
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AUTHORS
TITLE
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KEYWORDS
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/done lib="NIH MGC 254"
/clone lib="NIH MGC 254"
/note="Organ: brain/CNS; Vector: pExpress-1; Site_1:
ECORV; Site_2: Not1; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dT primer:
5-pGACTAGATCGAGAGGCGCCC(T)25-3' and cloned into
the ECORV/Not1 sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 2.18 kb. This
primary library is not normalized (normalized library is
NIH MGC 255) and was constructed by Express Genomics
(FrederIck, MD). Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Brain - Pooled from several tissues from one or more individuals" /lab_host="DH10B TonA"
Office of Cancer Genomics

National Cancer Institute / NIH

Bidg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.inh.gov

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1569 row: b column: 01

High quality sequence stop: 637.
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Musmalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Muschilla Butheria; Rodentia; Sciurognath; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (Dases 1 to 653)

Ckazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosama, H., Yangara, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batsel, K., W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gustincich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Malleis, L., Marchionni, L., McKenie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Sultana, R., Schneider, C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, S. Sultana, R., Schneider, C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, S. Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomte, M., Varagisawa, M., Yang, I., Yang, L., Yang, L., Wahlseved, J.C., Waynshaw-Boris, A., Yanagisawa, M., Yang, I., Hayatsume, M., Sato, K., Shiraki, Y., Konno, H., Nakawa, T., Pukuda, S., Hara, A., Hashizume, M., Inocani, K., Ishara, K., Satou, M., Sato, K., Shiraki, Y., Sasaki, D., Shibata, K., Shinagawa, M., Yasawa, I., Wayazaki, A., Sasaki, D., Sato, K., Shiraki, Y., Sasaki, D., Shibata, K., Shinagawa, M., Yasawa, I., Wayazaki, A., Sasaki, W., Sato, K., Shiraki, Y., Sasaki, Waterston, R., Land, Shinagawa, M., Yasawa, M., Yasawa, I., Yasunishi, A., Yasawizaki, Y., Sasaki, Y., Yasagisawi, M., Yasaka, Yasagisawi, M., Yasaka, Yasagisawi, M., Yasaka, Yasagisa, Yasagisawi, M., Yasaka, Yasagisawi, M., Yasagisawi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY727560 BYRN full-length enriched, adult male cortex Mus musculus cDNA clone B530005H20 5', mRNA sequence.
                                                                                                                             AAGATGGTGTCCCAGAGCTTCACCCAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCC 1369
                                                                                                                                                                                                                                                                                       1370 AAGTCGCTGGCCGTCATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCCATACACGCTGCTG 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1430 ATGATCATCCGGGCCGCCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGAAACCTCC 1489
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
                                                                                                                                                                                                            417
                                                                                                                                                                                                                                                                                                                                          537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 ATGATCATCCGAGCTGCTTGCCATGGCCGCTGCATCCCCGATTACTGGTACGAGACGTCC
                                                                                                                                                                           359 AAGATGGTGTCCCAGAGCATCACCCAGCGCTTCCGGCTGTCGCGGGAAG-AAGTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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BY727560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB611519 547 bp mRNA linear EST 07-APR-2003 AMGNNUC:NRHY3-00179-H8-A W Rat hypothalamus (10735) Rattus norvegicus cDNA clone nrhy3-00179-h8 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1069
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/clone lib="W Rat hypothalamus (10735)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; W Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                                                                                                                                   179 GGTGAGGCAGGCCCTGGTGTTGAGGCTGGGGAGGCTGCCCTCGGGGGTGGCAGTGGTGGA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                            CCTCGTCGCCCCTTCTGCATCCCACTGTATGTACCTACGTGCTGACAGGCCGCTGGAC
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                                                                                                                             517 GGATTCGAGCCTCCGCACCCAGAACAACTTCTTTCTGCTCAACCTCGCCATCTCCGACTT
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Plate: 00179 row: h column: 8.
Location/Qualifiers
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Pred. No. 1.1e-67;
0; Mismatches 72; Indels 7
                                                                                                                                                                                                                                                                                                                                                                   CTTCGGCCGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTAC 643

    .547
    organism="Rattus norvegicus"

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/db_xref="taxon:10116"
/clone="nrhy3-00179-h8"
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Amgen EST Program.
Amgen Rat EST Program.
Unpublished (2003)
Contact: Dan Fitzpatrick
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85.6%;
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AUTHORS
TITLE
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CB611519
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BF531112 409 bp mRNA linear EST 11-DEC-2000 602072279F1 NCI_CGAP_Brn67 Homo gapiens cDNA clone IMAGE:4215354
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NIH-MGC http://mgc.nci.nih.gov/.
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/clone_lib="NCI CGAP_BRNT CGAP_BRN5"
/note="Organ brain" Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Tncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN9790 row: m. column: 19
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                                                         181 GCCCCGCCGGCCAGCCAGCAGCAGCCCCTGCCCTGCCCAGTGTCCCCGAGCCCTGTGA
                                                                                                                                                                                                                                                       301 GCCGGAGAGGCGGCGGCTGCTGCTGCGCGCGCGCGCGTTTCTCGGCTGCCTGGCTGTC
                                                                                                                                                                            241 GCCTGCTGGCCGATGGAGCGCGCGCCCGACGGGCTGATGAACGCGTCGGGCGCTCTG
                                                                                                                                                                                                                            GCGGGCGATGCGGCGGCGGGCGGGCGGCGCGCGCTTCTCGGCAGCCTGGACCGGGTG
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4215354"
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BF531112
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                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/lab_host="DHIOB"
/lab_host="DHIOB"
/clone_lib="RIKEN full-length enriched, adult male cortex"
/clone_lib="RIKEN full-length enriched, adult was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research fund.
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Myrazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sasaxi,B., Sasaxi,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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/clone="B530005H20"
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Location/Qualifiers
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/strain="C57BL/6J"
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Query Match 13.8
Best Local Similarity 90.0
Matches 397; Conservative
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Job time: 8905.2 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8265
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@inage.llnl.gov). IMAGE ID= 1796445
Seq primer: M13 Forward.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                             CCTGGTGGCCAAGCCTGCCCGG-CACTCTGTTTGCTCACCCCAGGACCTCTGGGGGTTGT
                                                                                                                                                                                           2187 CCTAGGAACCTCGAAGCTGTTCTCTGCTTTTCCATTCTGGGTGTTTTCAGAAAGATGAAG
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate
Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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                                                             Score 386; DB 2; Length 409;
Pred. No. 9.6e-67;
0; Mismatches 5; Indels
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/mol_type="mRNA"
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                                                            14.3%;
98.5%;
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Best Local Similarity 98.5
Matches 400; Conservative
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/db xref="taxxon:10116"
/dlone="UI-R-B00-agr-c-06-0-UI"
/dev stage="adult"
/lab host="UI-R-B00"
/clone="UI-R-B00"
/clone="Vector: pT713D-Pac (Pharmacia) with a modified
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebellum,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.ulowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"
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/strain="Sprague-Dawley"
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

June Run on:

2, 2005, 05:05:49; Search time 5779.82 Seconds (without alignments) 11192.003 Million cell updates/sec

1 atggagcgcgccgcccga......ccctggagcactgctggaag 1335 US-10-727-021-6 1335 Perfect score: Sequence:

IDENTITY NUC Gapox 1.0 Scoring table:

9416466 Total number of hits satisfying chosen parameters:

4708233 segs, 24227607955 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

99 ba: *
99 bb: *
99 bb: *
99 con: * GenEmbl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AR135733 Sequence
BD235873 Isolated
AR217195 Sequence
BD235872 Isolated
AR317194 Sequence
AX549263 Sequence
AX549263 Sequence
AF140538 Homo sapi
AF311910 Homo sapi
AF31910 Homo sapi
AF31910 Homo sapi
AF31910 Homo sapi
AR104202 Sequence
BD086286 G protein
AR104201 Sequence
BD086286 G protein
CQ730452 Sequence
BD086286 G protein
CQ730452 Sequence Description AR217195 AR135732 BD235872 AR217194 AX549263 AF140538 AF321910 AB019000 Query Match Length DB 2699 2699 2699 2699 2699 1338 1362 2050 100.0 1332.4 1332.4 1332.4 1331.8 1331.8 1331.8 1331.8 Score Result No.

AKS59688 AB045369 AR104202 BD086286 AR104201 BD086285 CQ730452

2689 2665 1600

AF267537 Cavia por	AF237919 Rattus no	AR104204 Sequence	BD086288 G protein	AY009370 Rattus no	ARS59692 Sequence	AY142145 Mus muscu	AY044153 Mus muscu	AB015646 Rattus no	AR104203 Sequence	BD086287 G protein	BD189979 Use of hi	AF267538 Cavia por	AJ296652 Homo sapi	AL078633 Human DNA	AJ278250 Homo sapi	E39817 Novel guano	AR559681 Sequence	E39806 Novel guano	AR559670 Sequence	AY009371 Rattus no	E39809 Novel guano	AR559673 Sequence	AR104216 Sequence	BD086300 G protein	AR104215 Sequence	
AF267537	AF237919	AR104204	BD086288	AY009370	AR559692	AY142145	AY044153	AB015646	AR104203	BD086287	BD189979	AF267538	HSA296652	HS1005F21	HSA278250	E39817	AR559681	E39806	AR559670	AY009371	E39809	AR559673	AR104216	BD086300	AR104215	AT.TGNMENTS
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81.2	80.1	80.1	80.1	80.1	80.1	80.1	80.1	80.1	80.1	80.1	80.0	6.69	69.1	69.1	69.0	68.8	68.9	67.4	67.4	67.4	. 67.4	67.4	63.8	63.8	63.8	
1083.8	1069.2	1069.2	1069.2	1069.2	1069.2	1069.2	1069.2	1069.2	1069.2	1069.2	1067.6	932.6	923	923	921.4	919.8	919.8	899.2	899.2	899.2	899.2	899.2	852.2	852.2	852.2	
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

linear PAT 16-JUN-2001		Pyati,J. E the H3 subtype			Length 1335; Indels 0; Gaps 0;	3GGCGCTGGCGGCGATGCG 60	secectecececenter 60	CCGCGGTGCTGGCCGCGTC 120	cccccrcccccccrc 120	rggrcArgcrcgccrrcgrg 180	rggrcArgcrcGccrrcGrg 180	rCAACCTCGCCATCTCCGAC 240	CAACCTCGCCATCTCGAC 240	ACGTGCTGACAGGCCGCTGG 300
1335 bp DNA 6 from patent US 6136559. 1 GI:14476405	Unknown. Unknown. Unclassified.	Lovabes I CO 1333/ Lovenbergy T.W., Erlander,M., Huvar,A. and Pyati,J. DNA encoding as human histamine receptor of the H3 Patent: US 6136559-A 6 24-OCT-2000;	Location/Qualifiers 11335 /organism="unknown" 	Milet - Type - mideet gird Dis	100.0%; Score 1335; DB 6; larity 100.0%; Pred. No. 7.7e-178; Conservative 0; Mismatches 0;	ATGGAGCGCGCCCCCGACGGCCGCTGAACGCTTCGGGGGCGCTGGCGGGCG	ATGGAGGGCGCGCCCGACGGGCCGCTGATCGCTTCGGGGGCGCTGGCGGGGGGGATGCG	GCGGCGGCGGGGCGCGCGCGCTTCTCGGCAGCCTGGACCGCGGGTGCTGGCCGCGCTC	GCGCCGGCGCGCGCGCGCGCTTCTCGGCTGGACCGCGGGGGCGGGC	ATGGCGCTGCTCATCGTGCCCACGGTGCTGGCCAACGCGCTGGTCATGCTCGCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	ATGGCGCTGCTCATCGTGGCCACGGTGCTGCCTGGTCATGCTCGTCGTCGTCGTCGTCGTCGTGGTGCTTCGTG	GCCGACTCGAGCCTCCGCAGCAACTTCTTCCTGCTCAACCTCGCCATCTCCGAC	GCCGACTCGAGCCTCCGCACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGAC	TTCCTCGTCGGCGCCTTCTGCATCCCACTGTATGTACCCTACGTGCTGACAGGCCGCTGG
AR135733 Sequence 6 AR135733 AR135733.1	Unknown. Unknown. Unclassified.	Lovenberg, T.W., Lovenberg, T.W., DNA encoding as Patent: US 61365			덛	1 ATGGAGC	1 ATGGAGO				-			
RESULT 1 AR135733 LOCUS DEFINITION 5 ACCESSION 1 VERSION	WS 4		FEATURES SOUTCE	ORIGIN	Query Match Best Local Sir Matches 1335;			, 61	0 61	, 121	5 121	/ 181	0 181	7 241
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PAT 17-JUL-2003
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                                                                                                                                                                            other sequences; artificial sequences.

1 (bases 1 to 1335)
Labenberg,T.W., Erlander,M., Huber,A. and Piatei,J.

1solated DNA encoding human H3 histramine receptor
Patent: JP 2002556049-A 6 20-AUG-2002;

ORTHO MCNEIL PHARWACEUTICAL INC
OS Artificial Sequence
N JP 2002526049-A/6
PD 20-AUG-2002
PF 07-OCT-1998 JP 2000573370
PI TIMOTHY W LABENBERG,MARK ERLANDER,ARNE HUBER,JIYAXASYURY
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/organism='Artificial Sequence'
Location/Qualifiers
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/organism="synthetic construct"
//mol_type="genomic DNA"
/db_xref="teaxon:32630"
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Isolated DNA encoding human H3 1
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BD235873.1 GI:33045643
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BD235873
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DEFINITION
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                                                 TCTGCCTTCAACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCGAGCGGTC
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ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1335) AUTHORS Lovenberg, T.W., Erlander, M., Huvar, A. and Pyati, J. TILLE DNA encoding a human histamine receptor of the H3 subtype JONENAL Patent: US 6413743.4 6 02-JUL-2002; FEATURES 11335 SOURCE /organism="unknown" //mol_type="genomic DNA"	Query Match 100.0%; Score 1335; DB 6; Length 1335; Best Local Similarity 100.0%; Pred. No. 7.7e-178; Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps	Qy 1 ATGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	. Qy 61 GCGGCGGCGGCGCGCGCTTCTCGCAGCCTGAACCGCGGTGTTGTGGCCGCGCTC 1.	QY 121 ATGGCGCTGCTCATCGTGGCCACGGTGCTGGGCAACGCGCTGGTCATGCTCGCCTTCGTG 1.	Oy 181 GCCGACTCGACGCCCCGGACCCGGACTTCTTCCTGCTCAACCTCGCCATCTCCGAC 2.	QY 241 TTCCTCGTCGCCCTTCTGCATCCCACTGTATGTACCCTACGTGCTGACAGCCGCTGG 3	Oy 301 ACCTTCGGCCGGGCCTCTGCAAGCTGTGGTGGTGGTGGACTACCTGTGTGCACCTCC 3	Oy 361 TCTGCCTTCAACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGTCACCCCGAGCGGTC 4:	Qy 421 TCATACCGGGCCCAGGAGTGACACGGGGGGGGAGTGCGGAAGATGCTGCTGTGG 421 TCATACCGGGCCCAGGGGTGACACGCGGGGGGGGGGGGG	Qy 481 GTGCTGCCCTTCCTGCTGTACGACCAGCCATCCTGAGCTAGCT	Qy 541 AGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATC 6 b 541 AGCTCCATCCCCGAGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATC 6	OY 601 ACGCTTCCACCTGGAGTTCTTTACGCCCTTCCTCAGCGTCACCTTCTTTAACCTCAGC 6.	Oy 661 ATCTACCTGAACATCCAGAGGGGCACCCGCCTCCGGCTGGATGGGGCTCGAGAGGCACC 7:	Qy 721 GGCCCGGAGCCCCTCCCGAGGCCCAGCCTCACCCCCCACCGCCTGGCTGG	Qy 781 IGCTGGCAGAAGGGCACGGGGAGGCCATGCCGCTGCACAGGTATGGGTGAGGCG 8-	701 TOCTOR CARACTER GEORGE CONTROLL OF CONTROLL OF CARACTER CONTROLL OF CONTROL OF CON
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Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying surantispenic peptides
Patent: WO 02061087-A 548 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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Lovenberg, T.W., Erlander, M., Huvar, A. and Pyati, J.
DNA encoding a human histamine receptor of the H3 subtype
Patent: US 6413143-A 5 02-UUL-2002;
Location/Qualifiers
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100.0%; Pred. No. 6.7e-178;
ative 0; Mismatches 0;
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AR217194
AR217194.1 GI:23316634
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Homo sapiens histamine H3 receptor mRNA, complete cds.
AF140538
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Lovenberg, T.W., Roland, B.L., Wilson, S.J., Jiang, X., Pyati, J., Huvar, A., Jackson, M.R. and Erlander, M.G. Cloning and functional expression of the human histamine H3
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Lovenberg, T.W., Roland, B.R., Wilson, S.J., Jiang, X., Pyati, J.,
Huvar, A., Jackson, M.R. and Erlander, M.E.
Direct Submission
Submitted (GS-ARP-1999) Molecular Pharmacology, RW Johnson PR
3535 General Atomics Ct, San Diego, CA 92121, USA
Location/Qualifiers
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100.0%; Pred. No. 6.7e-178;
ive 0; Mismatches 0;
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IVATVIGNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTF
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CTGTGGGCCAACTGGGCTGTCAACCCTGTCCTCTACCCTCTGTGCCACCACCAGGCTTCCGC
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Takimura, T., Itadani, H. and Ohta, M.
Direct Submission
Submitted (20-00T-1998) Tetsuo Takimura, Banyu Pharmaceutical
Co., LTD, Tsukuba Research Institute; Okubo 3, Tsukuba, Ibaraki
300-2611, Japan (B-mail:takmratt@banyu.co.jp,
Tel:+81-298-77-2000(Gx:2251), Fax:+81-298-77-2027)
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/product="G-protein coupled receptor"
/protein id="BABA7030.1"
/db xref="GI:11022653"
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/organism="Homo sapiens"
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Novel G-protein coupled receptor
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                                                  GCGCCGCCGCGCGCGCGCTTCTCGGCACCTGGACCGCGGTGCTGCCCGCGCTC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases 1 to 2050)

I taya, K., Takimura, T., Nakamura, T., Kobayashi, M., Tana, K., Hidaka, Y. and Ota, M.

Novel guanosine triphospate (GTP)-binding protein-conjugate receptor protein

receptor protein

L. Patent: JP 2000189171-A 19 11-JUL-2000; BANYU PHARMACEUT CO LTD

OS Homo sapiens (human)

PN JP 2000189171-A/19

PP 25-MAY-1999 JP 1999145661

PR 25-DEC-1998 WO PCTJP9805967

PI KEI ITAYA, TETSUO TAKIMURA, TAKAO NAKAMURA, MASAHIKO KOBAYASHI, PI KENICHI TANAKA,
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C12P21/02,C12Q1/02,G01N33/15,G01N33/566,C12N15/00,C12N5/00 CC
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CI2N15/09, A61K45/00, C07K14/705, C12N1/15, C12N1/19, C12N1/21,
                                                                                              CGGGCCTTCACCAAGCTGCTCTGCCCCCAGAAGCTCAAAATCCAGCCCCACAGCTCCCTG
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Pred. No. 1.6e-177;
0; Mismatches 1;
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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Novel guanosine tri
receptor protein.
E39824
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GCGGCGGCGCGCGCGCGCTTCTCGGCAGCCTGGACCGCGGGGCTGCTGGCCGCGCTC
                                                                                                            GCCGACTCGAGCCTCCGCACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGAC
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                                ATGGCGCTGCTCATCGTGGCCACGGTGCTGGGCAACGCGCTGGTCATGCTCGCCTTCGTG
                                                  GCCGACTCGAGCCTCCGCAGCACCATCTTCCTGCTCAACCTCGCCATCTCCGAC
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Itadani, H., Takimura,T., Nakamura,T., Kobayashi,M., Tanaka,K.-I.,
Hidaka,Y. and Ohta,M.
Guanosine triphosphate (GTP) binding protein-coupled receptor
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Patent: US 6750322-A 21 15-UUN-2004;
Location/Qualifiers
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Co.,Ltd., Biomedical Labolatories; Okubo 3, Tsukuba, Ibaraki
300-2611, Japan (E-mail:itadnihr@banyu.co.jp, Tel:81-298-77-2000,
Fax:81-298-77-2027)
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Pred. No. 1.6e-177;
0; Mismatches 1; Indels 0;
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/codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (30-JUN-2000) Hiraku Itadani, Banyu Pharmaceutical
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AUTHORS Good TITLE Meth TOURNAL Pate	Goodeal, A. D.J. and Glucksmann, M.Alexandra. Methods for detecting nucleic acid molecules encoding a member of the muscarinic family of receptors Patent: US 609345-A 3 25-JUL-2000;	3 & 8	
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Perfect score:

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ALIGNMENTS

histamine H3 receptor; biogenic amine receptor homologue; ss. Human histamine H3 receptor open reading frame. AAA09062 standard; cDNA; 1335 BP. 98WO-US021090. 98WO-US021090. (first entry) WO200020011-A1. 07-OCT-1998; Homo sapiens. 07-OCT-1998; 10-AUG-2000 13-APR-2000. AAA09062; RESULT 1

(ORTH) ORTHO-MCNEIL PHARM INC.

Pyati J; Lovenberg TW, Erlander M, Huvar A, WPI; 2000-303632/26.

P-PSDB; AAY92218

polynucleotides and polypeptides used of receptor activity. The cDNA encodes the human histamine H3 receptor. The polypeptide Novel human histamine H3 receptor in methods to identify modulators Claim 2; Fig 2; 54pp; English.

contains the seven conserved hydrophobic domains and specific residues conserved in biogenic amine receptors. The human histamine H3 receptor polynucleotides and polypeptides are used in methods to screen for modulators of receptor activity (claimed). Such agonists and antagonists may prove useful as research tools or may be used as therapeutics to treat disorders directly or indirectly involving histamine receptors (claimed). The characterization of the polynucleotide is useful for forensic analysis, diagnostic applications, and epidemiological studies

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA molecules useful in gene therapy for the treatment of inflammation or allergy, or for encoding a human histamine H3 receptor and identifying histamine receptor modulators that are useful as therapeutic and diagnostic agents.
                                             TCCCAGAGCTTCACCCAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCCAAGTCGCTG
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              BP; 192 A; 476 C; 416 G; 251 T; 0 U; 0 Other;
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nootropic; neuroprotective; cerebroprotective; cardiant; antiasthmatic;
immunomodulator; gastrointestinal; antiallergic; antidiabetic;
antiinflammatory; hypotensive; antiarrhythmic.
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useful in identifying modulators of the human histamine H3 receptor,
which in turn are useful as therapeutic and diagnostic agents
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are agonists of recombinant human histemine H3 receptor protein activity, comprising combining a compound suspected of being an antagonist of human histamine H3 receptor protein activity with recombinant human histamine H3 receptor protein, and measuring an agonistic effect of the compound on the recombinant human histamine H3 receptor protein. The methods and compositions of the present invention are useful for diagnosing and treating human histamine H3 receptor-related disorders, such as central and peripheral nervous system disorders (depression, anxiety, psychoses, Parkinson's disease, Alzheimer's disease, dementia and tardive dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune, cardiovascular (hypertension, and arrhythmia) and gastrointestinal disorders. The present sequence is the coding sequence of the human histamine H3 receptor
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GCTTCACCCACCTCCAGCTCCGGCAGCTCCTGAGGGGCACTGAGAGGCCGCGCTCACTC
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                                                                                                                                                                                                                                                                                                                                      The invention relates to a monospecific antibody immunologically reactive with a protein appearing as ADD22854, where the protein functions as a human histamine H3 receptor. The antibody blocks intracellular signaling cativity of the human histamine H3 receptors in response to ligand binding. The antibody is useful for detecting and quantifying expression of human histamine H3 receptors, which may be useful for diagnostic, of human histamine H3 receptors, which may be useful for diagnostic, of human histamine H3 receptors, which may be useful for diagnostic, of pideniological or forensic purposes. The antibody is potentially useful in treating diseases such as depression, anxiety, schizophrenia, Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual Alzheimer's disease, obsesity, hypertension, Tourette's syndrome, sexual Alzheimer's disease, obsesity, hypertension, Tourette's syndrome, sexual cating disorders and anorexia, cardiovascular and cerebrovascular cating disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy, inflammation, or prostate dysfunction. The present sequence is the open cading frame encoding the histamine H3 receptor.
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                                                                                                                                               Huvar A, Pyati J,
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                                               21-AUG-2000; 2000US-00642514.
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                                                                                                                                               Lovenberg TW, Erlander M,
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P-PSDB; ADD22854.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a human histamine H3 receptor protein and nucleic acid encoding such protein. The invention is useful for identifying compounds that modulate the activity of human histamine H3 receptor. The invention is useful for treating a condition that is mediated by a human histamine H3 receptor in a patient and for treating extrinency discasse, obseity, Alzheimer's disease, pain, stress, ulcers, constipation and non-insulin dependent diabetes mellitus. The present sequence is a human histamine H3 receptor CDNA.
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Human; Parkinson's disease; obesity; Alzheimer's disease; pain; stress; ulcer; constipation; non-insulin dependent diabetes mellitus; gene; ss; histamine H3 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated and purified human histamine H3 receptor protein useful for identifying modulators utilized for treating Parkinson's disease, obesity, Alzheimer's disease, pain, stress or ulcers.
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                                                                                                                                                                                             histamine H3 receptor; biogenic amine receptor homologue; ss
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/product= "histamine_H3_receptor"
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                                                                                                                                            Human histamine H3 receptor cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the complete sequence of cDNA encoding a human histamine H3 receptor. The histamine H3 receptor DNA molecules are useful for isolating homologues of receptor, identifying and isolating genomic equivalents of receptor, and identifying, detecting or isolating mutant forms of the receptor. The DNA molecules are also useful in gene therapy for the treatment of inflammation or allergies. The human histamine H3 receptor protein is useful in identifying modulators of the human histamine H3 receptor, which in turn are useful as therapeutic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                          Complete nucleotide sequence of cDNA encoding a histamine
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                                                                                                                                                                Histamine; receptor; G-protein coupled receptor; human; neuroprotective; cardiant; antidepressant; tranquillizer; antiparkthoshinan; anorectic; hypotensive; analgesic; antidabetic; laxative; antiarrythmic; antiulcer; antiallergic; antiinflammatory; gene therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell prollferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis, allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypertension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
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                                                Human histamine H3 receptor nucleotide SEQ ID NO:548
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regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosolerosis, bacterial, fungal, processan or viral infections, osteoparterial, fungal, processan or viral infections, osteoparthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42569 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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100.0%; Pred. No. 3.3e-217;
tive 0; Mismatches 0;
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The present invention relates to a method of identifying compounds that are agonists of recombinant human histamine H3 receptor protein activity, comprising compound suspected of being an antagonist of human histamine H3 receptor protein activity with recombinant human histamine H3 receptor protein, and measuring an agonistic effect of the compound on the recombinant human histamine H3 receptor protein. The methods and compositions of the present invention are useful for diagnosing and treating human histamine H3 receptor-related disorders, such as central and peripheral nervous system disorders (depression, anxiety, psychoses, Parkinson's disease, Alzheimer's disease, dementia and tardive dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune, cardiovascular (hypertension, and arrhythmia) and gastroincestinal histamine H3 receptor
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nootropic; neuroprotective; cerebroprotective; cardiant; antiasthmatic;
immunomodulator; gastrointestinal; antiallergic; antidiabetic;
antiinflammatory; hypotensive; antiarrhythmic.
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The invention relates to a monospecific antibody immunologically reactive with a protein appearing as ADD22854, where the protein functions as a human histamine H3 receptor. The antibody blocks intracellular signaling cativity of the human histamine H3 receptors in response to ligand binding. The antibody is useful for detecting and quantifying expression of human histamine H3 receptors, which may be useful for disquestic, epidemiological or forensic purposes. The antibody is potentially useful in treating diseases such as depression, anxiety, schizophrenia, Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual cation, drug addiction or drug abuse, cognitive disorders, alzheimer's disease, obsessive-compulsive behaviour, panic attacks, pain, eating disorders and anorexia, cardiovascular and cerebrovascular cation disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy, inflammation, or prostate dysfunction. The present sequence is the full center of the companies of the full cannot be companied to the companied to the companied of the companied of the companied of the full center of the companied of the full center of the companied of the compan
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100.0%; Pred. No. 3.3e-217;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                         Pyati J;
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21-AUG-2000; 2000US-00642514
                                                                                                                                                                                                                                                                                                    Lovenberg TW, Erlander M,
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Best Local Similarity 100.
Matches 1335; Conservative
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P-PSDB; ADD22854.
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The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder. Or treating a subject having a urological disorder. Also described: (1) a method for identifying a subject having a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has urological disorder sare useful for identifying a polypeptides related to urological disorder; identifying a subject having a urological disorder. Disorder include urinary incontinence and benign prostatic disorder include urinary incontinence and benign prostatic related protein, which is used in the exemplification of the present
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                                                                                                                                                                        "urological disorder related protein 8203"
urological disorder; uropathic; cytostatic; urinary incontinence;
benign prostatic hyperplasia; human; gene; ss.
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                                                                                                          ocation/Qualifiers
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16-UUN-2003; 2003US-0478742P.
18-UUL-2003; 2003US-0488529P.
30-UUL-2003; 2003US-0491156P.
02-SEP-2003; 2003US-0499594P.
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2003US-0457901P.
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08-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a human histamine H3 receptor protein and uncleic acid encoding such protein. The invention is useful for feathfying compounds that modulate the activity of human histamine H3 receptor. The invention is useful for treating a condition that is mediated by a human histamine H3 receptor in a patient and for treating Parkinson's disease, obesity, Alzheimer's disease, pain, stress, ulcers, constipation and non-insulin dependent diabetes mellitus. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                      Human; Parkinson's disease; obesity; Alzheimer's disease; pain; stress; ulcer; constipation; non-insulin dependent diabetes mellitus; gene; ss; histamine H3 receptor.
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cive 0; Mismatches 0;
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Transgenic mouse; neurological disorder; adrenal gland disorder;

Colon disorder; intestinal disorder; immune disorder; bone disorder;

W muscular disorder; blood disorder; immune disorder; bone disorder;

Joint disorder; metabolic disorder; mutritive disorder; cancer;

W kidney disorder; uterus disorder; prostate disorder; testis disorder;

W ovary disorder; uterus disorder; pancreas disorder; septen disorder;

K thymus disorder; thyroid disorder; mutiparkinsonian; antimanic;

CNS; central nervous system; respiratory; antidiarrhoeic;

W cytostatic; antiinflammatory; vasotropic; antidiarrhoeic;

W intudée; hepatotropic; antibarderial; antidanginal; antidiabetic;

W dermatological; antiulcer; antibarderial; antidalergic; antidiabetic;

W dermatological; antidicer; antithyroid; antidialergic; numen;

mmunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids
                                                           <u>¢GGGCCGCCTGCCATGGCCACTGCGTCCCTACTGGTACGAAACCTCCTTCTGGCTC</u>
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                                                                                                  Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
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cof the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases, a transgenic computation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived comtation in a different GPCR gene of the invention; and kits comprising a nutation in a different GPCR gene of the invention. The probes which hybridise to GPCR polynucleotides of the invention. The comprising a GPCR mucleic acid. The GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, disease, distease or schizophrenia); chapteric neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., crohn's disease, diarrhoea, food poisoning or irritable bowel cyndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., autoimmune disorders or ADS); bone and joint disorders (e.g., autoimmune disorders or corteoporosis); metabolic or nutritive disorders or athritis, gout or osteoporosis; metabolic or nutritive disorders or chapters (e.g., cancers); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding mucleic acid of the invention. Note: The full sequence data for this
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Sequence 1338 BP; 193 A; 476 C; 418 G; 251 T; 0 U; 0 Other;

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SEX	Human G-pr	rotein conjugate-type receptor protein coding sequence.
	Guanosine G-protein muscarini blood pre	Guanosine triphosphate binding protein, signal transduction regulation; G-protein conjugate-type receptor protein; learning difficulty; BG2; muscarinic acetylcholine receptor; physiological function disorder; blood pressure; digestion; sleep; therapy; human; ss.
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                                                                                                                                                                                             This sequence encodes the human guanosine triphosphate binding protein (G-protein) conjugate-type receptor protein (designated BG2) of the invention. BG2 is a member of the G-protein conjugate-type receptor superfamily and shows significant homology to other muscarinic acetylcholine receptors. BG2 can be used in a screening method for identifying ligands binding to the BG2 receptor and for compounds which are agonists or antagonists to the binding of ligands to BG2 receptor, and which can be used for the regulation of signal transduction, and thus for the prevention and treatment of memory and learning difficulties and disorders of the control of physiological functions such as blood pressure, digestion and sleep
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                                                                                                                                              GTP binding protein conjugate-type receptor protein for screening candidate drugs for signal transduction modification.
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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CDNA Library Preparation: GPCR Consortium CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gow.b column: 06

organism="Homo sapiens"

/mol_type="mRNA" /db_xref="taxon:9606"

High quality sequence stop: 610. Location/Qualifiers 1. .732

> FEATURES SOURCE

Tissue Procurement: GPCR Consortium

2	4.4		775	σ	CC580463	CC5804	- М	CH240_375
9	3.6		1440	σ	AY404934	AY40493	_	Homo sapi
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0	1.6		975	-	AL536991	AL536		AL536991
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VERSION	CF14	CF147822.1	GI:33244090	244	060			
KEYWORDS	EST.							
SOURCE	Homo		ns (human)	an)				
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REFERENCE	1	(bases	1 to 732)	6				
AUTHORS	NIH	MGC ht	tp://mg	ŭ.	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	Nati	onal I	nstitut	68	of Health, Mam	malian Gene Collection		(MGC)
COMMENT	Cont	blishe act: D	Unpublished (1999) Contact: Daniela S.		Gerhard. Ph.D.			
	Offi	Office of Cancer						
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NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Note: this is a NIH MGC Library.
                                                             Score 677; DB 7; I Pred. No. 7.1e-125;
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1. .890
|/organism="Mus musculus"
|/mol_type="mRNA"
|/db xref="taxon:10090"
|/clone="IMAGE:5361966"
|/tissue_type="retina"
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|/lab_host="DH10B (phage-resistant)"
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|/lab_host="lab"NIH MGC 94"
|/lab_host="lab"NIH MGC 34"
|/lab_host="lab"NIH MGC 34"
|/lab_host="lab"NIH MGC 34"
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                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution at:
http://image.llnl.gov
Plate: LLAMI1920 row: m column: 07
High quality sequence stop: 811.
Location/Qualifiers
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
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AMGNNUC:URGP1-00001-D6-A urgpl (14349) Rattus norvegicus cDNA clone urgpl-00001-d6 5', mRNA sequence. CB556920 CB556920.1 GI:29496320 EST.
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                                                                                                                                                                                                                             729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 GCGGATTCGAGCCTCCGCACACCCAGAACTTCTTTCTGCTCAACCTCGCCATCTCCGAC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                         561 ACCCTGGAGTICTTTACGCCCTTCCTCAGCGTCACCTTCTTAACCTCAGCATCTACTG
CCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATCACGGCTTCC
                                                                                                           670 AACATCCAGAGGCGCACCCGCCTCCGGTGGATGGGGCTCGAGAGGCAGCCGGCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 GCGGCTGCAGGCGGGGGCGCGCTTCTCGGCTGCCTGGACCGCTGTCCTGGCTGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGACTCGAGCCTCCGCACCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCTCGTCGCCGCCTTCTGCATCCCACTGTATGTACCCTACGTGCTGACAGGCCGCTGG
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="urgp1-00001-d6"
/clone llb="urgp1 (14349)"
hoto="Vector: pSPORT1; Rat GPCR library rearrayed
internal pSPORT vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
Location/Qualifiers
1. 672
/organism="Rattus norvegicus"
/mol_type="manka"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                        | 130 | CCCCTCCCGAGGCCCAGCCTCACCACCCCCCCCG | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165 | 165
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 89.7
Matches 497; Conservative
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550
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CB556920
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                          1310
                                                                                                                                                                                                                                                                                                                                           CN423054 716 bp mRNA linear EST 16-MAY-2004
17000424504731 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
Mol type="mRNA"
/db xref="taxon:9606"
/tiSsue_type="embryonic stem cells, cell lines H1, H7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                             716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGGCCTCTGCAAGCTGTGGGTGGTGACTACCTGCTGTGCACCTCCTCTGCCTTC 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Tenbowski, J and Stanton, L.W.

Tenbowski, J and Stanton, L.W.

Transcriptome characterization

Control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 716)
                                               657 CAGCTTCCGTAGAGCCTTCACCAAGCTCCTCTGCCCCCAGAAGCTCCAAGGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCGGGGGGGTCTCATACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00
Location/Qualifiers
                                                                                                                                      1311 CAGCTCCCTGGAGCACTGCTGGAAG 1335
                                                                                                                                                                    717 TGGCTCCCTGGAGCAGTGCTGGAAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GRN_ES"
                                                                                                                                                                                                                                                                                                                                                                                                                               CN423054.1 GI:47410648
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                                                                                                                                                                                                                                                                                RESULT 3
CN423054
LOCUS
DEFINITION
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AMGNNUC:NRHY3-00179-H8-A W Rat hypothalamus (10735) Rattus norvegicus cDNA clone nrhy3-00179-h8 5', mRNA sequence. CBs11519.1 GI:29571407 EST.
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(Acganism="Rattus norvegicus"

// Acganism="Rattus norvegicus"

// Anol_type="mENA"

// Ab_xref="taxon:10116"

// Clone="nrhy3-00179-h8"

// Clone="rype="hypothalamus"

// Clone="lib="W Rat hypothalamus"

// Note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; W Rat hypothalamus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                          241 ATACACGCTGCTGATGATCATCCGGGCCGCCTGCCATGGCCACTGCGTCCTGACTACTG
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Plate: 00179 row: h column: 8.
Location/Qualifiers
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85.6%; Pred. No. 1e-67;
ive 0; Mismatches 72; Indels 7,
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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Amgen, Inc
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Amgen EST Program.
Amgen Rat EST Program
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1 (bases 1 to 910)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
High quality sequence stop: 601.
                                                                  ACCTTCGGCCGGGGCCTCTGCAAGCTGTGGCTGGTGGTAGACTACTACTGTGTGCCTCC
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Pred. No. 4.6e-72;
0; Mismatches 9; Indels 5
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/organism="Homo sapiens"
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Best Local Similarity 96.998
Matches 443; Conservative
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BE783826
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
7761: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.B. Consortium at
Seq primer: M13 Porward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF567596 499 bp mRNA linear EST 12-DEC-2000
UI-R-BOO-agr-c-06-0-UI.rl UI-R-BOO Rattus norvegicus cDNA clone
UI-R-BOO-agr-c-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                ATGAAGATGGTGTCCCAGAGCTTCACCCAGCGCTTTCGGCTGTCTCGGGACAGGAAGTG 1068
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cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library insmalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
                                                                                                                                                           28.9%; Score 385.4; DB 4
llarity 99.7%; Pred. No. 1.3e-66;
Conservative 0; Mismatches 1
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Rattus norvegicus
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Matches 386;
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AGENCOURT 6573270 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732210
5', mRNA Bequence.
BMS48665
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Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Invitrogen
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12733 row: p column: 03
High quality sequence stop: 654.
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1 (bases 1 to 1103)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab host="DH10B"
/clone lib="NIH MGC 124"
/note="forgan: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally
                                                           TGCTGGGGCTGCTGGCCAAAAGGGCATGGCGATGCCGTTGCACGGTATGGGGTG
                                                                                                                                                                                                                           AAGTCGCTGGCCATCATCGTGAGCATCTTTGGGCTCTGCTGGCGCGCCGTACACGCTCCTA
                                                                                                                  GGTGAGGCGGCCGTAGGCCGCTGAGGCCGGGGGGCGACCCTCGGGGGGTGGCGGTGGGGGC
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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BM548665
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
and minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1054
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Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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/lab_host="DH10B"
/clone_lib="MARC_1BOV"
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Plate: 108 row: H column: 13
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                     /Note="Vector: profile and profile and profile and polylinker; Site 1: Not 1; Site 2: Eco Ri; The library (UI-R-BOO) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebrallum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"
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1 (bases 1 to 519)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
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Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCCTCATCACGGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGCCTTCTGCATCCCATTGTACGTACCCTATGTGCTGACCGGCCGTTGGACCTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGGCCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCGAGCGGTCTCATACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCTGCTGTACGGACCAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGCAGCTCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 371.2; DB 2; Length
Pred. No. 8.2e-64;
0; Mismatches 44; Indels
                                                                                                                   /db_xref="taxon:10116"
/clone="UI-R-BO0-agr-c-06-0-UI"
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/clone_lib="UI-R-BO0"
                                        'organism="Rattus norvegicus"
                                                               /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACATCCAGAGGCGCACCGC 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 90.0°
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW669811
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
              source
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AUTHORS
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AW669811
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/clone="INGGE:58020702"
/tissue_type="neuroblastoma, cell line"
/lab host="MINGE:58020702"
/tissue_type="neuroblastoma, cell line"
/lab host="MINIO (phage-resistant)"
/clone lib="MINIM MGC 47"
/clone lib="Organ: brain; Vector: poTB7; Site_1: Xho1; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B. 1 (bases 1 to 946)

B. 1 (bases 1 to 946)

I. Unpublished (1999)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2037 row, i column: 07

High quality sequence stop: 678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ068856 946 bp mRNA linear EST 02-APR-2002
AGENCOURT_6740127 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802702
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                                                                                                                            718
                                                                                                                                                                                                                           772
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                                                                               789 CACGGGCTCCCACCTCGAGTTCTTCA-ACCCTTCCTCAGCGTTACCTTCTTCAACCTCAG 847
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                                                                                                                          CATCTACCTGAACATCCAGAGGCGCAC-CCGCCTCCGGCTGGATGGGGCTCGAGAGGCAG
                                                                                                                                                                                                                           719 CCGGCCCCGAGCCCCCTCCCGAGGCCCAGCCCTCACCACC-----CCCACCGCCTGGCT
                                                                                                                                                                                                                                                                         906 CTGGCCAATAAACCCCCACTGGAGCGCAAGCCTTGCCACCTCAGGTTCCCCCACATTGGT
                                                                                                                                                                                                                                                                                                                            773 GCTGGGGCTGCTGGCAGAAGGGGCACGGGGAGGCCATGCCGCTGCACAGGTATGGGGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA Sequence. B0068856
BQ068856.1 GI:19897902
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Best Local Si
Matches 331;
                                 600
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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BQ068856
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                                                                                                                                                 BQ950659 1046 bp mRNA linear EST 21-AUG-2002 AGENCOURT 8863943 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311932 5', mRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/db_xref=taxon:1090"
/clone="IMAGE:511932"
/lab_host="DHIOB (phage-resistant)"
/clone lib="NIH MGC 129"
/note="Organ: oIfactory epithelium; Vector: pCMV-SPORT6.1;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nth.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone through the I.M.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAM1375 row: k column: 05
High quality sequence stop: 640.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCTACCGGGCCCAGCAGGGGGACACAAGACGGGCTGTTCGGAAGATGGCACTGGTGTG 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGCTGGCCTTCCTGTGTATGGGCCTGGCATCCTGAGTTGGGAGTACCTGTCCGGTGG 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 CAACTCCATCCCGGAGGGCCACTGCTATGCTGAGTTCTTCTAC-ACTGGTACTTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTGCCTTCAACATCGTGCTCATCAGCTACGACCGCTTCCTGTCGGTCACCCGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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CCCCTACACACTCCTGATGATCATTCGGGCCGCCTGC 519
                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                  BQ950659.1 GI:22366137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1046
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Matches 472; Conserv
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AUTHORS
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JOURNAL
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                                                                                                   RESULT 10
BQ950659
                                                                                                                                                                                                                        ACCESSION
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Man Margaculus

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CE (bazk; Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Buscawa, Y., Mosgami, A.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mosgami, H.,

Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mosgami, H.,

Rume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Brade, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Kawaji, H., Kawaswa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglett, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ramachandran, S.,

Ravasi, T., Reed, J.C., Taylor, W.S., Tesadale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Walls, C., Wallming, L.G., Wanger, C., Wang, Y., Watanabe, Y.,

Wals, C., Wanger, L., Wahlestedt, C., Wang, Y., Rawa, J.,

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Ravasum, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Yoshiko, M., Sato, K., Shiraki, T., Yoshiko, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY727560 BYEN full-length enriched, adult male cortex Mus musculus CDNA clone B530005H20 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 GCGCTGCAGGCGCGCGCGCCTTCTCGCTGCTGCCTGGACCGCTGTCCTGGCTGCGTC
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                                                                                                                                                                                                                                                                                Gaps
NIH MGC 255) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"
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                                                                                                                                                                                     Length 842;
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                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                     DB 7;
                                                                                                                                                                                Score 294.4; DB 7
Pred. No. 1.8e-48;
0; Mismatches 32
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                                                                                                                                                                                     22.1%;
                                                                                                                                                                                     Query Match
Best Local Similarity 90.7
Matches 313; Conservative
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/lab host="MHING TonA"
/lab host="MHIN MGC 254"
/note="Organ: brain/CNS; Vector: pExpress-1; Site_1:
/note="Organ: brain/CNS; Vector: pExpress-1; Site_1: Si
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                                               61 AGTGGCCAAGTCGCTGGCCGTCATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 CCACCACAGCTTCCGCCGGGCCTTCACCAAGCTGCTCTGCCCCCCAGAAGCTCAAAATCCA 300
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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College of Wisconsin
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 01
                                                                                                                                                                                                                           121 GCTGCTGATGATCATCCGGGCCGCCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCTGATGATCATCCGGGCCGCCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Office of Cancer Genomics
National Cancer Institute / NIH
Bagi 31 RH0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B42 bp mRNA linear EST 01-4
AGENCOURT 27526928 NIH_MGC_254 Rattus norvegicus cDNA clone
CO403631315203 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1305 GCCCCACAGCTCCCTGGAGCACTGCTGGAAG 1335

    .842
    /organism="Rattus norvegicus"

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
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AUTHORS
TITLE
JOURNAL
COMMENT
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CO403631
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Gaps

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MEDLINE PUBMED COMMENT JOURNAL

TITLE

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AMGNNUC:SRTH1-00002-H10-A RDS RAT (13984) Rattus norvegicus CDNA CB758850
                                                                                            253 ATGGAGCGCGCCCCCGACGGCTGATGAACGCGTCGGGCGCTCTGGCCGGAGAGGCG 312
                                                                                                                                         61 GCGGCGGCGGGGGGGCGCGCGCGTTCTCGGCAGCCTGGACCGCGGTGCTGGCCGCGCGCTC 120
                                                                                                                                                               121 ATGGCGCTGCTCATCGTGGCCACGGTGCTGGCAACGCGCTGGTCATGCTCGCCTTCGTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="srth1-00002-h10"
/cell_type="artificial construct"
/clone_lib="RDS RAT" (13984)"
/note="artificial construct for rat sequencing requests"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGAGCGCGCCCCCGACGGCCGCTGAACGCTTCGGGGGCGCTGGCGGCGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch al Similarity 91.5%; Pred. No. 3.6e-44; Pred. No. 3.6e-44; 289; Conservative 0; Mismatches 27; Indels
    57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 TCTGCCTTCAACATCGTGCTCATCAGCTACGACCGCTTC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 ---AGTCTCAACATCGTGCTGATCAGCTATGACCGATCC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
    0; Mismatches
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Plate: 00002 row: h column:
Location/Qualifiers
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
       Matches 336; Conservative
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2011) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                     Email: genome_ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Sano,H., Saeski,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Pred. No. 5.4e-45;
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/clone="B530005H20"
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                                                                                                                 Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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/lab_host="DH10B"
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374 CCTGGACGGTCTTCCTGGCTGTCCTGATGGGGGTCCTCATAGTTAGCACCGTGCTGGGGA 433
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Job time: 4404.8 secs
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IMAGE:6949081 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/lone_lib="NICHD_XGC_EPTO:
/none="Organ: eye; Vector: pCNV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
GCGGCTGCAGGCGCGCGCGCGCTTCTCGGCTGCCTGGACCGCTGTCCTGGCTGCCTC
                                                                     GCGGATTCGAGCCTCCGCACCCCAGAACAACTTCTTTCTGCTCAACCTCGCCATCTCCGCCA
                                                  ATGCCCTCCTCATCGTGCCCACGCTGCTGGCCAACGCGCTGGTCATGCTCGCCTTCGTG
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov f column: 24
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NHH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RanloA07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
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Xenopus laevis
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/mol_type="mRNA"
/db_xref="taxon:8355"
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Location/Qualifiers
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335 TAGTGGACTACCTGCTGTGCACCTCCTGCCTTCAACATCGTGCTCATCAGGACC 394
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155 ACGCGCTGGTCATGCTCGCCTTCGTGGCCGACTCGAGCCTCCGCACCCCAGAACAACTTCT
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The human histamine H3 receptor contains the seven conserved hydrophobic domains and specific residues conserved in biogenic amine receptors. The human histamine H3 receptor polynucleotides and polyreptides are used in methods to screen for modulators of receptor activity (claimed). Such agonists and antagonists may prove useful as research tools or may be used as therapeutics to treat disorders directly or indirectly involving histamine receptors (claimed). The characterization of the polynucleotide is useful for forensic analysis, diagnostic applications, and
Novel hum
Human H3
Murine hi
Mouse GPC
Rat G pro
Rat G-pro
Rat H3ta
Rat hista
Rat Hista
Rat H1 rat
Human H3
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G-protein
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N-PSDB; AAA09061, AAA09062.
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Score 2361; DB 3; Length 445; Pred. No. 3.1e-181;

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Gaps

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Histamine, receptor, G-protein coupled receptor; human. neuroprotective; cardiant; antidepreseant; tranguillizer; antiparkinosinian; anorectic; hypotensive; analgesic; antidiabetic; laxative; antiarrythmic; antiulcer; antiallergic; antilnflammatory.
of receptor, identifying and isolating genomic equivalents of receptor and identifying, detecting or isolating mutant forms of the receptor. DNA molecules are also useful in gene therapy for the treatment of inflammation or allergies. The human histamine H3 receptor protein is useful in identifying modulators of the human histamine H3 receptor, which in turn are useful as therapeutic and diagnostic agents
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                                                                                                             100.0%; Score 2361; DB 4; Length 445; 100.0%; Pred. No. 3.1e-181;
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                                                                                        61 ADSSLRTQNNFFILNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLMLVVDYLLCTS
                                                                                                                                      GPEPPPEAQPSPPPPGCWGCWQKGHGBAMPLHRYGVGBANGBABAGBATLGGGGGGGGGSV
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                                        ADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
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                          MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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  Indels
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N-PSDB; AAC62366.
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                                                                                                            Novel isolated and purified DNA molecule encoding human histamine H3 receptor protein, useful for identifying modulators of human histamine H3
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  Pyati J;
  Huvar A,
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  Erlander
                                           2002-641560/69
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  Lovenberg TW,
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The present invention relates to antibodies specific for human histamine receptor protein subclasses H1, H2 and H3. These antibodies prevent histamine binding to the receptors and can be used to prevent and treat allergic reactions and inflammatory diseases. The present sequence is the human H3 receptor
                                                                                                                                                 Human, histamine receptor; H1; H2; H3; antigen; antibody; antiallergic;
antiinflammatory; immunosuppressive; allergy; inflammatory disease.
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                                                                                                            Human histamine receptor subclass H3 protein.
AA019746 standard; protein; 445
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2002DE-01013916.
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28-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular GPCR or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR., and in the production of specific antibody against a particular GPCR, and in the production of specific antibody. The peptides and antibodies. The peptides for GPCRs are useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for creating immune-related diseases, growth-related diseases, call reading immune-related diseases, growth-related disease, call creating immune diseases, immunologial-related disease, call creating immune diseases, immunologial-related disease, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, catheroscall, fungal, protozoan or viral infections, osteoarchritis, osteoarchis, fungal, protozoan or viral infections and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, anxiety, depression, schizohrenia, dementia, mental retardation, memory closs, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoarosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; traumä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                   Human histamine H3 receptor protein SEQ ID NO:549.
                                                   421 RAFTKLLCPQKLKIQPHSSLEHCWK 445
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                                                                                                                                                                                                    ABP81687 standard; protein; 445
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                                                                                                                                                                                                                                                                                                                                                                                            61 ADSSERTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                    1 MERAPPOGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                          Length 445;
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                                                                                                                                                                  ; Score 2361; DB 6;
; Pred. No. 3.1e-181;
0; Mismatches 0;
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WPI; 2003-168704/17.

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This invention describes a novel antibody that is specific for a histamine receptor protein (HRP), especially human, and is able to inhibit binding of histamine to HRP. The antibody is produced by immunisation with an antigenic polypeptide that comprises (i) an extracellular domain (BCD) having a sequence from the first extracellular compress (ii) an extracellular domain (BCD) having a sequence from the Nereminus of the third transmembrane region (TMP) having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a sequence from the second BCL and optionally a TMD having a BCD having a sequence from the second BCL and optionally a TMD having a BCD having a sequence from the second BCL and optionally a TMD having a BCD having a sequence from the second BCL and optionally a TMD having a BCD having a sequence from the second BCL and option from the disclosure of the invention haman histamine
                                                                                 New antibody specific for histamine receptor protein, useful for treating or preventing e.g. allergy or inflammation, also antigens for its
                                                                                                                                                                                                                                                        Claim 2; Fig.2C; 14pp; German.
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Sequence 445 AA;

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100.0%; Score 2361; DB 6; Length 445; 100.0%; Pred. No. 3.1e-181; tive 0; Mismatches 0; Indels 0
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The present invention relates to a method of identifying compounds that are agonists of recombinant human histamine H3 receptor protein activity, comprising a compound suspected of being an antagonist of human histamine H3 receptor protein activity with recombinant human histamine H3 receptor protein activity with recombinant human histamine H3 receptor protein. The methods and compositions of the present invention are useful for diagnosing and treating human histamine H3 receptor-related disorders, such as central and peripheral nervous system disorders (depression, anxiety, psychoses, parkinson's disease, Alzheimer's disease, dementia and tardive dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune, cardiovascular (hypertension, and arrhythmia) and gastrointestinal disorders. The present sequence is the human histamine H3 receptor
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                                    Human; histamine H3 receptor; receptor modulator; agonist; nootropic;
neuroprotective; cerebroprotective; cardiant; antiasthmatic;
immunomodulator; gastrointestinal; antiallergic; antidiabetic;
antiinflammatory; hypotensive; antiarrhythmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying agonists of recombinant human histamine H3 receptor gactivity, useful for diagnosing and treating H3 receptor-related disorders, such as nervous system disorders, asthma, allergy, hypertension and diabetes.
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100.0%; Pred. No. 3.1e-181;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                             (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                  15-NOV-2001; 2001WO-US045313.
                                                                                                                                                                                                                                                                                         15-NOV-2001; 2001WO-US045313.
  Human histamine H3 receptor.
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Best Local Similarity 100.
Matches 445; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-457595/43.
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                                                                                                                                                                      WO2003044059-A1.
                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       Lovenberg T;
                                                                                                                                                                                                            30-MAY-2003
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ABP59931 standard; protein; 445

RESULT 7

28-AUG-2003 (first entry)

ABP59931;

ABP59931 ID ABP XX AC ABP XX DT 28-

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New polynucleotide encoding a human H3 histamine receptor polypeptide, useful for diagnosing or treating disorders associated with or modulated by H3 histamine receptor, e.g. depression, anxiety, obesity, hypertension or diabetes.
                                     420
                                                       The invention relates to splice variants of human H3 histamine receptor polypeptide and their corresponding polynucleotide sequences. The invention is useful in diagnosing or treating diseases or disorders associated with or modulated by the H3 histamine receptor, such as central nervous system disorders (e.g. depression, anxiety, psychoses, Parkinson's disease or Alzheimer's disease), obesity, hypertension, Tourette's syndrome, sexual dysfunction, gastrointestinal disorders (e.g. constipation), drug addiction, cardiovascular or cerebrovascular disorders (e.g. arrhythmia), diabetes, stress, ulcers, asthma, allergy, inflammation and prostate dysfunction. It is also used in gene therapy. The polypeptide is useful for identifying agonists, antagonists or inverse agonists of histamine action at the H3 receptor. The present sequence is human wild-type H3 receptor protein
ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL 360
                                                                                                                                                                                                                                                                                                                                                                           Human; H3 histamine receptor; central nervous system, depression; ulcer; Tourette's syndrome; sexual dysfunction; drug addiction; cardiovascular; anxiety; Parkinson's disease; Alsener's disease; obesity; arrhythmia; constibation; gastrointestinal disorder; inflammation; cerebrovascular; diabetes; hypertension; stress; allergy; prostate dysfunction; asthma;
                                   AVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
                                                                                                                                                                                                                                                                                                                                            Human wild-type H3 receptor (H3a) protein.
                                                                                                        RAFTKLLCPQKLKIQPHSSLEHCWK 445
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                                                                                                                                                                                                                                                                                                        (first entry)
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N-PSDB; AAL59976.
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61 ADSSERTQNNFFELNLAISDFLVGAFCIPLYVPYVLIGRWIFGRGLCKLWLVVDYLLCTS
                                                                                                                 241 GPEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGGSV
                                                                                                                                                                                                                                                                                   SAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG
                                                                                                                                                        SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
                                                                                                                                                                                  SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
                                                                                                                                                                                                                                                                     ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL
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                                                                                                                                                                                                                                                                                                                                         New antibody against human histamine H3 receptor, preferably with receptor antagonist activity, useful for diagnostic purposes and for treating diseases such as depression, Parkinson's disease, obesity or
                                                                                                                                                                                                               GPEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSV
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                                                                                                                                                                                                                                                                                                                                                                                  421 RAFTKLLCPQKLKIQPHSSLEHCWK 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD22854 standard; protein; 445
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N-PSDB; ADD22860, ADD22861.
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1 MERAPPOGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV 60

Match 100.0%; Score 2361; DB 7; Length 445; Local Similarity 100.0%; Pred. No. 3.1e-181; es 445; Conservative 0; Mismatches 0; Indels 0;

Matches 445; Conservative

Query Match

Eliasof SD

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Use of polypeptides related to urological disorders, e.g. 44390, 5. 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 132; 542pp; English,
                                                                                                                                                                                                                                                  Karicheti V, Silos-Santiago I,
                                                                                04-FEB-2003; 2003US-0444783P.

27-MAX-2003; 2003US-0457901P.

08-MAX-2003; 2003US-0468775P.

19-MAX-2003; 2003US-0471614P.

16-UIN-2003; 2003US-048822P.

30-UIL-2003; 2003US-0491156P.
                                           14-JAN-2004; 2004WO-US000750.
                                                                                                                                                                                 02-SEP-2003; 2003US-0499594P.
26-SEP-2003; 2003US-0506332P.
                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
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                                     with a protein appearing as ADD22654, where the protein functions as a main with a protein appearing as ADD22654, where the protein functions as a activity of the human histamine H3 receptor in response to ligand binding. The antibody is useful for detecting and quantifying expression of human histamine H3 receptors, which may be useful for diagnostic, epidemiological or forensic purposes. The antibody is potentially useful in treating diseases such as depression, anxiety, schizophrenia, Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual dysfunction, drug addiction or drug abuse, cognitive disorders, pain, attacks, obsessive-compulsive behaviour, panic attacks, pain, eating disorders and anorexia, cardiovascular and cerebrovascular disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy, inflammation, or prostate dysfunction. The present sequence represents the histamine H3 receptor.
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                            invention relates to a monospecific antibody immunologically reactive
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                                                                                                                                                                                                                                                                              100.0%; Score 2361; DB 7; Length 445; 100.0%; Pred. No. 3.1e-181; ive 0; Mismatches 0; Indels 0
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SEQ ID NO 7; 25pp; English
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The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorder is urological disorder, identifying a compound capable of treating a urological disorder, identifying a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence represents a human urological disorder related protein, which is used in the exemplification of the present
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100.0%; Pred. No. 3.1e-181
:ive 0; Mismatches 0;
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Matches 445; Conservative
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Best Local Similarity
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ADSSLRTQNNFFLLMLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, Parkinson's disease; obesity; Alzheimer's disease; pain; stress;
ulcer; constipation; non-insulin dependent diabetes mellitus;
histamine H3 receptor; receptor.
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AVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
                                                                                       AVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
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100.0%; Pred. No. 3.1e-181;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human histamine H3 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                               ADR31458 standard; protein; 445 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUVA/) HUVAR A. (PYAT/) PYATI J.
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                                                                SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGARBAA
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MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV

antidepressant; antiarrythmic; antidiabetic; antlinflammatory;

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phosphatidylinositol turn-over and signalling), secretion of a molecule phosphatidylinositol turn-over and signalling), secretion of a molecule (e.g. a neurotransmitter or a glandular enzyme), or contraction of a smooth muscle cell, treat disorders mediated by abnormal mACHR-6 activity e.g nervous system disorders (e.g. amnesia, apraxia, agnosia, amnestic Alabeimer's related memory loss and learning disability, visual hallucinations, perceptual disturbances, and Lewry body dementia associated delirulm), schizo-effective disorders (e.g. schizophrenia with mood swings, and depressive illness, paradoxical sleep abnormalities, disorders (e.g. REM sleep abnormalities, paradoxical sleep abnormalities, and body temperature or respiratory depression abnormalities during sleep), pain generating mechanism disorders (e.g. related to Parkinson's disease), eating disorders (e.g. insulin hypersecretion related obesity), drinking disorders (e.g. insulin hypersecretion related obesity), drinking disorders (e.g. disorters eigher polydipsia), smooth muscle related disorders (e.g. IBS, diverticular disease, urinary incontinence, oesophagaal achalasia, and chronic obstructive airways disease), cardiac disorders (e.g pathologic bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and chronical disorders (e.g pathologic bradycardia or tachycardia, arrhythmia flutter and fibrillation), and glandular disorders (e.g. xerostomia and diabetes mellitus)
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Sequence 445 AA;

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                                                             1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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99.8%; Score 2357; DB 2; Length 445; 99.8%; Pred. No. 6.5e-181; ive 1; Mismatches 0; Indels
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G protein coupled receptor; flh84g5; human; diagnosis; screening; therapy; antiparkinsonian; nootropic; neuroprotective; neuroleptic;
                                                                                                                        Human G protein coupled receptor flh84g5.
                AAY06322 standard; protein; 445 AA.
                                                                                     06-SEP-1999 (first entry)
                                                    AAY06322;
AAY06322
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                     ocation/Qualifiers
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    phosphatidylinositol.
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              Homo sapiens.
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New nucleic acid encoding an isolated G-protein coupled receptor useful for treating nervous system related disorders.

Claim 8a; Fig 1; 140pp; English.

The present sequence represents a novel human G protein coupled receptor, termed filh84g5, as deduced from a human cerebellum cDNA clone (see AAX39167). The invention provides human, rat and mouse filh84g5 concerned filh84g5 and antisense human cerebellum cDNA clone (see polymucleotides (including polymucleotides encoding the transmembrane regions of filh84g5 and antisense nucleic acid molecules), expression concerned antibodies, and a method of modulating phosphatidal propeptides and antibodies, and a method of modulating phosphatidal filh84g5 polypeptides can (i) interact with a filh84g5 ligand, such as cactylcholine or carnitine, (ii) interact with a filh84g5 ligand, so realistum channel (e.g. a calcium activated chloride channel or a potassium con channel (iv) modulate cytosolic ion, e.g. calcium concentration, (v) modulate cytosolic ion, e.g. calcium concentration, (v) modulate the release of a neurotransmitter, e.g. cactylcholine or carnitine from a neuron, (vi) modulate a filh84g5 ligand concentration, (v) modulate the release of a neurotransmitter, e.g. cactylty. The products can be used to treat: disorders mediated by corposphatialylinositol turnover, and (vii) modulate phospholipase C actylty. The products can be used to treat: disorders system related conspirated disorders, e.g. amnesia, apraxia, agnosia, amnestic spatial disorientation, Kluver-Bucy syndrome, Alzheimer's related memory constrained disorientation, Ruver-Bucy syndrome, Alzheimer's related memory constrained and learning disability; disorders affecting consciousness such as visual hallucinations, perceptual disturbances or delerium associated with Lewy body dementia, apraxia, agnosia, amnestic suffective consisted such as REM sleep abnormalities in patients suffective depression, paradoxical alsep abnormalities in patients suffective depression, paradoxical alsep abnormalities in patients suffective disorders and paramined and disorders affecting pain generation mechanisms e.g. pain related to irritable bowel syndrome or chest pain; movement disorders e.g. Parkinson's disease related movement disorders; eating disorders e.g. insulin hypersecretion related obesity or drinking disorders, e.g.

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diabetic polydipsia; smooth muscle related disorders, e.g. irritable bowel syndrome, diverticular disease, urinary incontinence, oesophageal achalasia or chronic obstructive airways disease; cardiac muscle disorders, e.g. pathologic bradycardia or tachycardia, arrhythmia, flutter or fibrillation; and gland related disorder such as xerostomia or diabetes mellitus. The products can also be used for detection, diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; muscarinic acetylcholine receptor 6; mACHR-6; detection; antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidiabetic; antidecessant; antiarrhythmic; antiinflumatory; carnifine; pain; G-protein coupled receptor; nervous system related disorder; xerostomia; disorders affecting consciousness; affective disorder; movement disorder; irritable bowel syndrome; drinking disorder; gland related disorder; smooth muscle related disorder; cardiac muscle disorder; diababetes mellitus; diagnosis; drug screening.
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                                                                                                                                                                   1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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                                                                                                                    Length 445;
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                                                                                                                                            Indels
                                                                                                                     Score 2357; DB 2;
Pred. No. 6.5e-181;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG67830 standard; protein; 445 AA
                                                                                                                    99.8%;
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                                                                                                                                            datches 444; Conservative
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                                                                                                                    Query Match
Best Local Similarity
                                                                        and drug screening
                                                                                               Sequence 445 AA;
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The present sequence represents human muscarinic acetylcholine receptor 6

(mACHR-6), which is a member of the G family of proteins. mACHR-6 has
antiparkinsonian, noctropic, neuroprotective. neurologic, antidiabetic
antidepressant, antiarrhythmic neuroprotective. neurologic, antidiabetic
antidepressant, antiarrhythmic neuroprotective. The mACHR
c protein, is capable of modulating the effects of a G-protein coupled
c receptor (GPCR) ligand such as acetylcholine or an acetylcholine like
molecule such as carnitine, e.g. by modulating phospholipase C
signalling/activity. Products from the present invention can be used for
treating disorders mediated by abnormal mACHR-6 protein activity such as
c rereptor system related disorders disorders affecting
c pain generation mechanisms such as pain related to irritable bowel
c syndrome or chest pain, movement disorders, cardiac muscle disorders, and
disorders, smooth muscle related disorders, cardiac muscle disorders, and
c disorders such as xerostomia or diabetes mellitus. The
products can also be used for detection, diagnosis and drug screening.
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99.8%; Pred. No. 6.5e-181;
ive 1; Mismatches 0;
                                                                                                                                       197. 219
/label= transmembrane_domain
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transmembrane_domain
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                                                                                 152. .174
/label= transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00165543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goodearl ADJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-394858/33.
N-PSDB; AAH44572, AAH44573.
                                                                                                                                                                                                                                                            .416
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17-MAR-1998;
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The present invention describes aminoazetidine, pyrrolidine and piperidine derivatives (1), which are used for the treatment of disorders and diseases related to the histenine H3 receptor. (I) have anorectic, and diseases related to the histenine H3 receptor. (I) have anorectic, and anotopic, antidiabetic, antiallerain, antiemetic, antidiate, ontidiate, antilipaemic, cardiant, osteopathic, antiarthritic, auditory and cytostatic activities. (1) can be used for treating and/or preventing diseases and disorders related to H3 histamine receptor e.g. overweight or obesity, eating disorders (e.g. bullimia and binge eating), impaired glucose tolerance, type 2 diabetes, allergic rhinitis, ulcer, anorexia,
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GPEPPPEAQDSPPPPPGCWGCWQKGHGEAMPLHRYGVGBAAVGAEAGEATLGGGGGGGGSV
                                  GPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGSV
                                                                                                                                                                    AVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
                                                                                                                                  ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL
                                                                                                                                                                                                                                                                    AVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histamine H3 receptor; aminoazetidine; pyrrolidine; piperidine; anorectic; anabolic; antidiabetic; antiallergic; antiinflammatory; antiulcer; nootropic; neuroprotective; tranquilliser; antianfemetic; antiatehmatic; antilipaemic; cardiant; osteopathic; antiarthritic; auditory; cytostatic; overweight; obesity; eating disorder; bulimia; bings eating; impaired glucose tolerance; tyrp 2 diabetes; ulcer; allergic rhinitis; anorexia; Alzheimer's disease; narcolepsy; artention deficit disorder; Alzheimer's disease; narcolepsy; irritable bowel syndrome; gall bladder disease; cancer; narcolepsy; cerneinon deficit disorder; airway disorder; asthma; dyslipidaemia; coronary heart disease; osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        RAFTKLLCPQKLKIQPHSSLEHCWK 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human histamine H3 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR43667 standard; protein; 445 AA
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16-MAY-2002; 2002DK-00000750.
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ABR43667
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Alzheimer's disease, narcolepsy and attention deficit disorder, for the delaying or preventing the progression from non-insulin requiring type 2 diabetes. for reducing weight and subpressing appetite or satisfy induction. (I) can also be used for treating dementia, motion sickness, vertigo, irritable bowel syndrome, gall bladder disease, cancer of breast, prostate and colon, narcolepsy, attention deficit disorder, airway disorders (e.g. asthma), dyslipidaemia, coronary heart disease and osteoarthritis. (I) have high and selective binding affinity to the histamine H3 receptor. The present sequence represents the human histamine H3 receptor protein, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                     1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
                                                                                                                                                                                                                                                                                                                                                                                                          1 MERAPPOGPLNASGALAGEAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSV
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                                                                                                                                                                                                                                                                                                  99.8%; Score 2357; DB 6; Length 445; 99.8%; Pred. No. 6.5e-181; ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAFTKLLCPQKLKIQPHSSLEHCWK 445
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein June Run on:

2, 2005, 19:07:00 ; Search time 24 Seconds (without alignments) 1784.019 Million cell updates/sec

1 MERAPPDGPLNASGALAGDA......LLCPQKLKIQPHSSLEHCWK 445 US-10-727-021-7 2361 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	histamine H4 recep	muscarinic recepto	muscarinic acetylc			muscarinic acetylc	muscarinic acetylc		muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	alpha-2-adrenergic		muscarinic acetylc	muscarinic acetylc octopamine recepto	muscarinic acetylc octopamine recepto tyramine receptor										
	ai	JC7566	151837	A29514	809508	A24325	A31897	S47572	S01114	S10128	B29514	S10127	833776	C29514	JT0530	JH0197	A29476	S10856	JT0531	A40972	S10126	A27386	A55019	A38316		A35546	A35546 JH0170	A35546 JH0170 S12004
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, 2	!	30.7	25.1	25.1	25.1	24.9	24.5	23.4	23.1	22.9	22.8	22.7	22.7	22.6	22.3	22.3	22.3	22.2	'n	4	21.9	ä	21.6	21.4	21.3			
	Score	724	592	592	591.5	œ	578	553.5	4	541	539	536	535	532.5	527.5	525.5	525.5	524.5	523.5	~	517.5	~	511	505.5	504		98.	98.
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317

373 PYTLLMITRAACHGHCVP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKLLCPQK 431

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alpha-2 adrenergic

2 I49481

450

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alpha-2-C2 adrener	alpha-2A-adrenergi	alpha-2-adrenergic	muscarinic acetylc	alpha-2B-adrenergi	alpha-2 adrenergic	alpha-2-adrenergic	alpha-2B-adrenergi	alpha-2B-adrenergi	alpha-2B-adrenergi	alpha-2-adrenergic	histamine H1 recep	G protein-coupled	alpha 2C4 adrenoce	G protein-coupled	histamine H1 recep
S28221	A34169	B40392	S48657	151883	I49480	A40392	A37223	A37869	A35642	. OH0190	A41632	JC5042	A48392	558868	JC1415
N	7	~	7	~	~	7	7	~	~	~	7	~	~	~	~
455	450	450	484	448	458	458	450	458	453	450	491	476	458	484	486
20.5	20.5	20.4	20.3	20.2	20.2	20.2	20.0	20.0	19.9	19.8	19.8	19.8	19.7	19.7	19.7
485	484.5	480.5	479	478	478	478	473	472	469	468.5	468	467	466	466	466
4															

ALIGNMENTS

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histenaine H4 receptor, HH4R - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: JG7566
R;Adamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.
B;Odhem. B.ophys. Res. Commun. 279, 615-620, 2000
A;Title: Molecular Cloning and characterization of a new human histamine receptor, HH4R.
A;Contents: Leukcyte
A;Contents: Leukcyte
A;Accession: JG7566
A;Aolecule type: man.
A;Residues: 1-390 cNAXA
A;Residues: 1-390 cNAXA
A;Residues: UNIPROT: Q9H3NB; DDBJ:AB045370
C;Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
30.7%; Score 724; DB 2; Length 390;
Best Local Similarity 38.6%; Pred. No. 1.3e-43;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps
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A;Cross-references: UNIPROT:P08482
R;Bonner, T.1; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
A;Recession: A94293
A;Molecule type: mRNA
A;Reperimental Source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequence
R;Rutrenbach, E.; Curits, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J; Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A;Reference number: A37121; MUID:90337982; PMID:2380182
A;Accession: A37121
A;Status: preliminary
A;Molecule type: protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphog
F;25-50/Domain: transmembrane #status predicted <TM3>
F;62-50/Domain: transmembrane #status predicted <TM3>
F;142-168/Domain: transmembrane #status predicted <TM4>
F;142-168/Domain: transmembrane #status predicted <TM4>
F;142-168/Domain: transmembrane #status predicted <TM5>
F;167-209/Domain: transmembrane #status predicted <TM5>
F;20-12/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SPTSSSGSSSRGT-ERPRSLKR-----GSKPSASSASLEKRMKWVSQSFT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 AVRKMLLVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPF 211
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S09508; S06327; S04326
R;Chapman, C.G.; Browne, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 WQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSLACADLIIGTFSMNLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 --VTVM-CTLYWRIYRETENR---ARELAALQGSETPGKGGGSSSSERSQPGAEGSPES
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Best Local Similarity 33.7%; Pred. No. 2.8e-34;
Matches 149; Conservative 66; Mismatches 149; Indels
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                                                                                                                                                                                                                                                                            muscarinic receptor - rat

GiSpecies: Rattus sp. (rat)

GiSpecies: Rattus sp. (rat)

GiSpecies: Rattus sp. (rat)

GiSpecies: Rattus sp. (rat)

GiAccession: 151837

Rilai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roes)

Rilai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roes)

Ayrille: The molecular properties of the MI muscarinic receptor and its regulation of Ayreference number: 151837

Ayrille: The molecular properties of the MID:1759615

Ayreference number: 151837

Ayreference number: 1518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPG-CWGC-------WQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSVA- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A94518; A94293; A37121; A29514
R;Bonner, T.I.
submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: A94518
A;Accession: A94518
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 VPYVLJGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSVTFFNLSIYLNIQRRTRLRLDGAREAA---GPEPP-------PEAQPSPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 KMPMVDSEAQAPTKQPPKSSPNTVKRPTKKGRDRGGKGQKPRGKE-QLAKR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 WQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSLACADLIIGTFSMNLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGRCCRCRAPRILIQAYSWKEEEEE----DEGSMESLTSSEGEEP-----GSEVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SPTSSSGSSSRGT-ERPRSLKR-----GSKPSASSASLEKRMKMVSQSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRFRLSRDRKVAKSLAVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W-TAVLAALMALLIVATVLGNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVRKMLLVWVLAFILYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 25.1%; Score 592; DB 2; Length 46
Best Local Similarity 33.7%; Pred. No. 2.8e-34;
Matches 149; Conservative 66; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVNPMCYALCNKAFRDTFRLLL 433
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IKKQP 379
                    436
                LKIOP
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Muscarinic acetylcholine receptor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Sacession: A24225

R;Kubo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; Hage
Nature 323, 411-416, 1986

A;Tille: Cloning, sequencing and expression of complementary DNA encoding the muscarinic

A;Reference number: A24325; MUID:87014801; PMID:3762692

A;Reference number: A24325; MUID:87014801; PMID:3762692

A;Residues: 1-460 cKUB>
A;Residues: 1-460 cKUB>
A;Residues: UNIPROT:P04761; GB:X04413; NID:g1863; PIDN:CAA28003.1; PID:g1866

C;Superfamily: vertebrate rhodopsin

C;Keywords: G procein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphop

C;Keywords: G procein-coupled receptor; glycoprotein; neurotransmitter ransmembrane #status predicted <TM1>
F;62-50/Domain: transmembrane #status predicted <TM3>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;100-121/Domain: transmembrane #status predicted <TM5>
F;107-209/Domain: transmembrane #status predicted <TM5>
F;107-209/Domain: transmembrane #status predicted <TM5>
F;107-30/Domain: transmembrane #status predicted <TM5>
F;107-
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C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 24-Nov-1999
C;Accession: A31897
C;Accession: A31897
S;Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, B.M.; Nathanson, N.M.
J. Biol. Chem. 263, 18397-18403, 1988
A;Title: Isolation, sequence, and functional expression of the mouse MI muscarinic acetyl
A;Reference number: A92694; MUID:89054021; PMID:2848036
A;Accession: A31897
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGGSS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 IPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA-- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 DEGSMESLISSEGEEP-----GSEVVIKMPMVDPEAQAPAKQPPRSSPNTVKRPTRKG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 RERAGKGOKPRGKE-QLAKR------KTPSLVKEKKAARTLSAILLAFIVTWTPYNI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 SSLRTONNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS-LKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSLAVIVSIFGLCWAPYTL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 QGSETPGKGGGSSSSERSQPGAEGSPETPPGRCCRCCRAPRLLQAYSWKEEEEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYGVGEAAVGAEAGEATLGGGGGGGSVA-------SPTSSSGSSSRGTERP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 587.5; DB 2; Length 31.8%; Pred. No. 5.8e-34; ive 73; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity ... Matches 150; Conservative
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A; Roblecule type: DNA
A; Residues: 1-460 - ALL>
A; Coss-references: GB:Y00508; GB:M35128; NID:g297405; PIDN:CAA68560.1; PID:g297406
B; Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929; J1987
A; Reference number: S04326; MUD:88166632; PMID:3443095
A; Reference number: S04326; MUD:88166632; PMID:3443095
A; Reference number: S04326; MUD:88166632; PMID:3443095
A; Reference number: S04326; MUD:88166632; PMID:343334.1; PID:g32318
A; Residues: 1-172, M', 174-460 - PER>
A; Robidues: 1-172, M', 174-460 - PERS
A; Robidues: 1-172, M
Nucleic Acids Res. 18, 2191, 1990
A;Title: Isolation of the human ml (Hml) muscarinic acetylcholine receptor gene by PCR a A;Fitle: Isolation of the human ml (Hml) muscarinic acetylcholine receptor gene by PCR a A;Reference number: 809508; MUID:90245684; PMID:2336407
A;Accession: 809508
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuas: 1-460 cCHA>
A;Cross-references: UMIPROT:P11229; EMBL:XS2068; NID:934450; PIDN:CAA36291.1; PID:934451
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
A;Note: the nucleotide sequence of the gene encoding the human MI muscarinic acetylcholine receptor.
A;Reference number: 806327; MUID:88096607; PMID:3697105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS-LKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSLAVIVSIFGLCWAPYTL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 151; Conservative
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Muscarinic acetylcholine receptor M2, glandular - pig
Mylernate names: muscarinic acetylcholine receptor III
Cispecies: Sus scrofa domestica (domestic pig)
Cibate: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
CiAccession: S01114
RiAkiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
FEBS Lett. 235, 257-261, 1988
A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonic A;Reference number: S01114; MUID:88296835; PMID:3402600
A;Accession: S01114
A;Molecule type: DNA
A;Residues: 1-590 -AKI>
A;Residues: 1-590 -AKI>
A;Cross-references: UNIPROT:P11483; EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate status predicted <TM1>
F;105-125/Domain: transmembrane #status predicted <TM3>
F;105-125/Domain: transmembrane #status predicted <TM3>
F;105-125/Domain: transmembrane #status predicted <TM3>
F;105-105/Domain: transmembrane #status predicted <TM3>
F;105-105/Do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AEQMDQDHSSSDSWNNNDAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSTILNSTKL 383
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                                                                                                                                                                                                                                                      89 VIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMNLFTTYIIMNRWALGNLACDLWLSID
                                                                                                                                                                                                                                                                                                                                                 115 YLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSW
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444 NSSVGKTTAT-LPLSFK------EATLAKRFALKTRSQITKRKRMSLIKEKKAAQTLS
                                                                             5 PPD-----GPLNASGALAGDAAAAGGAR----GFSAAWTAV-LAALMALLIVATVLGNAL
                                                                                                                                                30 PPGTVTHFGSYNISRA-AGNLSSPNGTTSDPLGGHTIWOVVFIAFLTGVLALVTIIGNIL
                                                                                                                                                                                                            55 VMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 VIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PPD-----GPLNASGALAGDAAAAGGAR----GFSAAWTAV-LAALMALLIVATVLGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------GEAT-----
              Gaps
          86; Mismatches 175; Indels 139;
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26.6%;
              149; Conservative
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A;Residues: 1-460 <SHA>
A;Note: the authors translated the codon ATC for residue 119 as Thr
A;Note: the authors translated the codon ATC for residue 119 as Thr
B;Shadi.co. R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 264, 6596, 1989
A;Reference number: A92742
A;Reference number: A92742
A;Reforence number: A92742
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc F;55-50/Domain: transmembrane #status predicted <TM1>
F;62-93/Domain: transmembrane #status predicted <TM4>
F;187-209/Domain: transmembrane #status predicted <TM6>
F;187-209/Domain: transmembrane #status predicted <TM6>
F;367-387/Domain: transmembrane #status predicted <TM7>
F;402-420/Domain: transmembrane #status predicted <TM7>
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C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPG-CWGC------WQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSVA- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPGRCCRCCRAPRLLQAYSWKEEEEE-----DEGSMESLITSSEGEEP------GSEVVI 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVRKMLLVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 W-TAVLAALMALLIVATVLGNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SPTSSSGSSSRGT-ERPRSLKR----GSKPSASSASLEKRMKMVSQSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.5%; Score 578; DB 2; Length 460; 33.0%; Pred. No. 2.7e-33; ive 68; Mismatches 150; Indels
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Pred. No. 1.8e-31;
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-590 <LEE>
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A,Accession: B94293
A,Rolecule type: manNA
B,Ruttenbach, E.; Cuttis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
B,Ruttenbach, E.; Cuttis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
A,Ritle: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A,Reference number: A37121; MUID:90337982; PMID:2380182
A,Rocession: B37121
A,Status: preliminary
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Aymolecule type: protein
Aymolecule type: protein
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Cysupardamily: vertebrate rhodopsin
Cysupardamily: vertebrate rhodopsin
Cysupardamily: vertebrate rhodopsin
F;67-90/Domain: transmembrane #status predicted <TMM>
F;67-90/Domain: transmembrane #status predicted <TMM>
F;142-163/Domain: transmembrane #status predicted <TMM>
F;142-163/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 SEQMDQDHSSSDSWNNNDAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSTILNSTKL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ASPT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 PSSDNLQVPEEELGMVDLERKADKLQAQKSVDDGGSFPKSFSKLPIQLESAVDTAKTSDV 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQS-FTQRFRLS--RDRKVAKSLA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 VIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFRR 421
  VMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVD 114
                                                                                                           YLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSW 174
                                                                                                                                                                                                              EYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLD 234
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R, Bonner, T.I.
submitted to GenBank, July 1987
A, Reference number: A94518
A, Accession: B94518
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A; Residues: 1-589 <BO1>
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Mome sapiens (man)
Cispecies: Mome sapiens (man)
Cispecies: Momentary structures, ligand-binding properties and tissue-specific expra A; Title: Distinct primary structures, ligand-binding properties and tissue-specific expra A; Residues: 1-590 vers.
A; Residues: 1-590 vers.
A; Residues: 1-590 vers.
A; Residues: 1-590 vers.
A; Coss-references: UNIPROT: P20309; EMBL: X15266; NID: 932323; PIDN: CAA33337.1; PID: 932324
A; Coss-references: UNIPROT: P20309; EMBL: X15266; NID: 932323; PIDN: CAA33337.1; PID: 932324
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F; 105-131/Domain: transmembrane #status predicted <TM2>
F; 105-131/Domain: transmembrane #status predicted <TM3>
F; 131-252/Domain: transmembrane #status predicted <TM5>
F; 131-252/Domain: transmembrane #status predicted <TM5>
F; 252-264f/Domain: transmembrane #status predicted <TM5>
F; 252-464f/Domain: transmembrane #status predicted <TM5>
F; 252-464f/Domain: transmembrane #status predicted <TM5>
F; 252-464f/Domain: transmembrane #status predicted <TM5>
F; 252-64f/Domain: transmembrane #status predicted <TM5-
F; 252-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSSDNLQVPEEELGTVDLERKASKLQAQKSMDDGGSFQKSFSKLPIQLESAVDTAKASDV 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- ASPT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQS-FTQRFRLS--RDRKVAKSLA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFRR 421
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149 YVASNASVANLLVISPDRYFSITRPLTYRAKR-TTKRAGVMIGLAWVISFILWAPAILFW
                                                                                                                                                                                                                                                                                              EYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLD
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A;Accession: S33776
A;Molecule type: DNA
A;Residues: 1-479 <KND>
A;Residues: 1-479 <KND>
A;Crossidues: 1-479 <KND>
C;Crossidues: 1-479 <KND
C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 RKKKROMAARERKVTRIIFAILLAFILIWIPYNVMVLVNTFCQS-CIPDIVWSIGYWLCYV 444
                                                                                                                                                                                                                                                                        128 ISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGGSSIPEGH 187
                                                                                                                                                                                                                                                                                                                                                                                                                           ------PEPPP----EAQPSP--PPPPGCWGCWQKGHGEAMPLHR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ADKDT----SNESSSGSATQNTKERPATELSTTEATTPAMPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
                                                                                                                                                                                                                                 68 ONNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNIVL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRL---RLDGAREAAG--- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AFLKSPLMKQSVKKPPPGEAAREELRNGKLEEAPPPALPPPP-------RPV-- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: :| | : | : | : | | CFIQFLSNPAVTFGTAIAAFYLPVVIMTV--LYIHISLASRSRVHKHRPEGPKEKKAKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 YGVGEAAVGAEAGEATLGGGGGGSVASPTSSSGSSSRGTE----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRFR--LSRDRKVAKSLAVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWA
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                                                                             9 PLN-ASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFVADSSLRT
                                                                                                                                                   6 PVNGSSGNQSVRLVTSSSHNRYETVEMVFIATVTGSLSLVTVVGNILVMLSIKVNRQLQT
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       130; Conservative 101; Mismatches 150; Indels 126; Gaps
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Local Similarity 25.9%; Pred. No. 3e-30;
les 127; Conservative 96; Mismatches 174; Indels
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muscarinic acetylcholine receptor m4 - mouse
C;Species. Mus musculus (house mouse)
C;Decies. Mus musculus (house mouse)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text
C;Accession: $33776; $33135
C;Accession: $33776; $33135
B;van Koppen, C.J.; Lenz, W.; Nathanson, N.M.
Biochim. Biophys. Acta 1173, 342-344, 1993
A;Title: Isolation, sequence and functional expression o
A;Reference number: $33776; MUID:93305731; PMID:7916637
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F.402-422/Domain: transmembrane #status predicted <TM5>
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F;434-455/Domain: transmembrane #status predicted <TM7>
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A; Residues: 1-479 < PER>
A; Cross = references: UNIPROT: P08173; EMBL: X15265; NID: 932321; PIDN: CAA33336.1; PIDS: 93232
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc
F; 32-57, Domain: transmembrane #status predicted < TM3>
F; 70-94, Domain: transmembrane #status predicted < TM4>
F; 192-216, Domain: transmembrane #status predicted < TM6>
F; 401-422, Domain: transmembrane #status predicted < TM6>
F; 401-422, Domain: transmembrane #status predicted < TM6>
F; 433-456, Domain: transmembrane #status predicted < TM6>
F; 401-422, Domain: tran
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10127
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, 1
EMBO J. 6, 3923-3929, 1987
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expecience number: S04326; MuID:88166632; PMID:3443095
                                                                                                                                                                                                                                                                                                                                                                                     CIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQ 146
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                                                                                                                    predicted
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F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status
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Pred. No. 2.5e-30;
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Best Local Similarity
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Matches 127; Conservative 96; Mismatches 158; Indels 125; Gaps 9 PLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFVADSSLRTQ	Qy 69 NNFFLLNLAISDFLVGAFCIPLYVPYUTGRWIFGRGLCKLWLVVDYLLCTSSAFNIYLI 128 : : -: : : : : : :	OY 129 SYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGGSSIPEGHC 188	Oy 189 YABFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAAG 241 ::	Oy 242PBPPPBAQPSPPPPPGCWGCWQKGHGEAMPLHRY 275	Qy 276 GVGEAAVGAEAGEATLGGGGGGSVASPTSSSGSSSRGTE	QY 316RPRSLKRGSKPS	Qy 347 RFRLSRDRKVAKSLAVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLMAN 404 i	RESULT 14 UT0530 WINGCAINIG acetylcholine receptor M5 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Detcies: J-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000 C;Accession: VT0530 R;Bonner, T.I.: Young, A.C.; Brann, M.R.; Buckley, N.J. Neuron 1, 403-410, 1988 A;Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor A;Residues: 1-532 -8DN> A;Residues: 1-532 -8DN> A;Residues: 1-532 -8DN> C;Commant: Muscarinic acetylcholine receptors mediate many of the actions of the neurotre C;Superfamily: vertebrate rhodopsin C;Commant: Muscarinic acetylcholine receptor; glycoprotein; neurotransmitter receptor; phosphog F;O-93/Domain: transmembrane #status predicted <tm3> F;O-157/Domain: transmembrane #status predicted <tm3> F;O-157/Domain: transmembrane #status predicted <tm3> F;144-64/Domain: transmembrane #status predicted <tm3> F;144-64/Domain: transmembrane #status predicted <tm3> F;144-64/Domain: transmembrane #status predicted <tm3> F;147-64/Domain: transmembrane #status predicted <tm3> F;</tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3></tm3>
66 NNYFLFSLACADLIIGAFSWNLYTLYIIKGYWPLGAVVCDLWLALDYVVSNASVWNLLII 129 SYDRFLSVTRAVSYRAQQGDTRRAVRKWLLVWVLAFLLLYGPALLSWEYLSGGSSIPEGHC	Qy 189 YARFFYNWYFLITASTLEFFTPFLSVTFFNLSYYLNIQRRTRLRLDGARRAAG 241 ::	Qy 242PEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLHRY 275	Oy 276 GVGEAAVGAEAGEATLGCGGGGSVASPTSSSGSSSRGTERPRSLKRGSKPS-327	Oy 328	Qy 360 LAVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSF 419 1	Qy 420 RRAFTKLLCPQ 430 1:	RESULT 13 C29514 muscarinic acetylcholine receptor M4 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999 C;Accession: C94518; C94293; E37121; C29514	submitted to GenBank, July 1987 A; Reference number: A94518 A; Reference number: A94518 A; Residues: 1-478 - 801- B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Bonner, T. T.; Buckley, N. J.; Young, A. C.; Brann, M.R. B; Reference number: A94293 A; Molecule type: mRNA A; Residues: 1-231, 731-7478 A; Note: only a part of the protein translation is given; none of the nucleotide sequence A; Rote: only a part of the protein translation is given; none of the nucleotide sequence A; Rote: only a part of the protein translation A; Reference number: A37121; MUID: 90317982; PMID: 2380182 A; Altiel: Muscarinic acetylcholine receptors, Peptide sequencing identifies residues invo A; Reference number: A37121; MUID: 90337982; PMID: 2380182 A; Molecule type: protein A; Residues: 68-130 < KUR- C; Superfamily: vertebrate rhodopsin C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphot C; Keywords: G protein-coupled receptor; glycoprotein, neurotransmitter receptor; phosphot C; Keywords: G protein-coupled receptor; glycoprotein, resonamenbrane #status predicted < TM3> F; 191-56/Domain: transmembrane #status predicted < TM3> F; 191-210/Domain: transmembrane #status predicted < TM3> F; 191-210-213/Domain: transmembrane #status predicted < TM3> F; 191-214/Domain: transmembrane #status predicted < TM3> F; 191-215/Domain: transmembrane #status predicted < TM3> F; 191-215/Domain: transmembrane #status

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60 YFLFSLACADLIIGVFSMNLYTLYTVIGYWPLGPVVCDLWLALDYVVSNASVMNLLIISF 119
                                                                    DRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYA 190
                                                                                                    289 VSAVASNWRDDEITQDENTVSTSLGHSRDDNSKQTCIKIVTKAQKGDVYTPTSTTVELVG 348
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Job time: 26 secs
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| 1,23-48 Domain: transmembrane #status predicted <TM1> |
| 1,29-16 Domain: transmembrane #status predicted <TM2> |
| 1,29-16 Domain: transmembrane #status predicted <TM3> |
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| 1,29-16 Z Domain: transmembrane #status predicted <TM5> |
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A;Residues: 1.466 <LAI>
A;Residues: 1.466 <LAI>
A;Residues: 1.466 <LAI>
A;Rutrenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, B.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo
A;Reference number: A37121; MUID:90337982; PMID:2380182
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26.8%; Pred. No. 1.3e-29;
tive 94; Mismatches 170; Indels 91; Gaps 12;
236
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267 NQASWSSSRRSTSTTGKPSQATGPSANWAKAEQLTTCSSYPSSEDEDKPATDPVLQVVY- 325
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C;Accession: JH0197, D37121
R;Lai, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A;Title: Amplification of the rat m2 muscarinic receptor gene by the polymer
A;Reference number: JH0197; MUID:91041524; PMID:2172674
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Residues: 60-122 «KUR»
Superfamily: vertebrate rhodopsin
Keywords: G protein-coupled recept
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Matches 130; Conservative
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Listing first 45 summaries
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    protein search, using sw model

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       Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570
564
553.5
548.5
                                                                                  Perfect score:
Sequence:
                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                              1919
1919
1521
1521
1223
1186
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688.5
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                                                                                                                                                                                                                                                                                                                                                                                                                     860
                              OM protein
                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                 Searched:
                                                                                                                                                                                                                      Database
                                             Run on:
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pongo pygma
gorilla gor
                                                                                               homo sapien
pan troglod
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                                                                                                                                                                                                                                                                                                                                          sapien
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                                                                                                                                                                                                                                                    rattus norv
                                                                                                                                                                                                                                                                                                                 homo sapien
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MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021:3550279;
Goge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,
Aacia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.;
"Genomic organization and characterization of splice variants of the
                                                                                                                                                                                                                                                                                                                                             homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
MEDLINE=20569725; PubMedel1111834; DOI=16.1006/bbrc.2000.4008;
NAKABULT T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
"Molecular Cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21953383; PubMed-11956964; DOI-10.1007/s007020200036; Wiedemann P., Boenisch H., Oerters F., Bruess M.; "Structure of the human histanaine H3 receptor gene (HRH3) and identification of naturally occurring variations."; J. Neural Transm. 109:443-453 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 3).
Ullmer C., Zirwes E., Lubbert H.;
"Cloning and functional expression of the human histamine H3S
"receptor.",
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                    Q8vh25
Q96rg8
P08173
P32211 r
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Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
receptor.";
P11483
Q661i8
Q7t286
P20309
                                                                                                                     09n2a4
09n2a2
09n2a3
096rg9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9YSN1; Q9GZX2; Q9H4K8; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 25-CT-2004 (Rel. 45, Last annotation update) Histenaine H3 receptor (HH3R) (G protein-coupled receptor 97) Home-BRH3; Synonyms-GPCR97; Home sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor, HH4R.";
Biochem. Biophys. Res. Commun. 279:615-620(2000).
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                                                                                         ACM3 HUMAN
ACM3 PANTR
ACM3 PONPY
ACM3 GORGO
Q96RG9
                                                                                                                                                                                                                                                                                                                                       ACM4 HUMAN
ACM4 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                       ACM5 MACMU
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Q8VHZ5
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                                                                                                                                                                                                                                                                                                                 Q96RG8
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Mammalia, Butheria, Primates;
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Biochem. J. 355:279-288(2001)
      SEQUENCE FROM N. TISSUE=Thalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
      2. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5. 46. 5.
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SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

A Dolusas P., Matchaws L.H., Ashurst J.L., Butron J., Gilbert J.G.R.,

Jones M., Stavrides G. Almeida J.P., Babbage A.K., Bagguley C.L.,

Basley J., Barlow K.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Buck D., Burrill W.D., Blakey S.E., Bridgeman A.M., Brown A.J.,

Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Ammond S., Harley J.L., Heath P.D., Ho S., Holden P.J.,

Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvacelaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Shownkeen R.,

Skuce C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R.,

Skuce C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R.,

Skuce C.D., Smith M.L., Taylor R., Tee D., Thomas D.W., Thorpe A.,

Skuce C.D., Smith M.L., Wallis J.M.,

Mhitchead S.L., Whittaker P., Willey D.L., Thilliams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whittehead S.L., Whiteher P., Willey D.L., Williams L.,

Walliming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R.,

Wall M., Boders J.:
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Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414.865-871(2001).
Is the following the following sequence of the following sequence of adenjate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist). Agonist stimulation of isoform 3 niether modified adenjate cyclase activity nor induced intracellular calcium

mobilization. SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS: ++

Event=Alternative splicing; Named isoforms=7; Comment=Additional isoforms seem to exist;

IsoId=Q9Y5N1-1; Sequence=Displayed; Name=1

IsoId=Q9Y5N1-2; Sequence=VSP_001886; Name=3; Synonyms=H3S; IsoId=Q9Y5N1-3; Sequence=VSP_001885; Name=2;

IsoId=Q9Y5N1-4; Sequence=VSP_001881; Name=4;

IsoId=Q9YSN1-5; Sequence=VSP_001882;

IsoId=Q9Y5N1-6; Sequence=VSP_001883;

TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the greatest expression in the thalamus and caudate nucleus. The various isoforms are mainly coexpressed in brain, but their relative expression level varies in a region-specific manner. Isoforms 3 and 7 are highly expressed in the thalamus, caudate nucleus and cerebellum while isoforms 5 and 6 show a poor expression. Isoforms 5 and 6 show a high expression in the amygdala, substantia nigra, cerebral cortex and hypothalamus. Cerebral cortex and hypothalamus. Isoform 7 is not found in hypothalamus or substantia nigra.

-!- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome [MIM:146500]. This syndrome is characterized by orthostatic hypothanion, bladder and bowel incontinence, anhidrosis, iris atrophy, amystrophy, ataxia, rigidity and tremor.

-!- MISCELLANEOUS: Does not bind to cimetidine and tripolidine. Shows modest affinity for thioperamide, imetit, N-alpha-methylhistamine and R(-)-alpha-methylhistamine. Isoforms 1 and 3 bind it with high affinity. Cerebral coupled receptor 1 family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ô GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004969; F:histamine receptor activity; TAS.
GO; GO:000197; P:G-protein signaling, coupled to cyclic nucl. . ; TAS.
GO; GO:0007269; P:neurocransmitter secretion; TAS. Gaps PEAM; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODDSN.

PRINTS; PR01471; HISTAMINEH3N.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

Alternative splicing; Disease mutation; G-protein coupled receptor; N-linked (GlcNAc. . .) (Potential). Missing (in isoform 4). /FIIda-Sp_001881. Missing (in isoform 5). ö | FTIGEASP 001885. | K -> KKOMKKKTCL (in isoform 2). | FTIGEASP 001886. | A -> V (in Shy-Drager syndrome). | FTIGEASR 012235. | E -> D (in Ref. 1 and 5). Query Match 99.8%; Score 2357; DB 1; Length 445; Best Local Similarity 99.8%; Pred. No. 2.9e-126; Matches 444; Conservative 1; Mismatches 0; Indels 0 Extracellular (Potential). Extracellular (Potential) Extracellular (Potential) -> D (in Ref. 1 and 5). 2ACF7440FBE95B6C CRC64; Extracellular (Potential) Cytoplasmic (Potential). Cytoplasmic (Potential). Cytoplasmic (Potential). Cytoplasmic (Potential) /FTId=VSP 001883. Missing (In isoform 7). /FTId=VSP 001884. Missing (In isoform 3). Missing (In isoform 6). Potential. Potential Potential Potential Potential Poly-Ala. Potential Potential Poly-Gly InterPro; IPR000276; GPCR_Rhodpsn. InterPro; IPR003980; H3_receptor. EMBL; AP140538; AAD38151.1; -...
EMBL; AB045569; BAB20090.1; -...
EMBL; AAD396652; CAC51025.1; -...
EMBL; AJ78256; CAC51025.1; -...
EMBL; AL078653; CAC39434.1; -...
EMBL; AL078633; CAC39434.1; -... 19 19 E 445 AA; 48671 MW; EMBL; AL078633; CAC04014.1; EMBL; AF363791; AAK50040.1; Transmembrane. HGNC:5184; HRH3. 39 60 70 70 70 1129 1177 1177 1196 2117 2117 4116 445 23 256 298 11 11 98 315 342 263 353 445 280 234 274 197 227 MIM; 604525; -. Glycoprotein; MIM; 146500; TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN DOMAIN TRANSMEM SEQUENCE /ARSPLIC /ARSPLIC VARSPLIC VARSPLIC RANSMEM /ARSPLIC ARSPLIC CONFLICT VARIANT DOMAIN Genew; DOMAIN DOMAIN DOMAIN

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1 MERAPPOGPLNASGALAGEAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P58406;
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                                                                                                                                                                                                                                                                                                                                                           420
 9
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

R EMBL; AV213164; AA063757.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0004859; F:histamine receptor activity; IEA.

R GO; GO:000186; F:receptor activity; IEA.

R InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR000376; TECEPTOR.

R Pfam; PF00001; 7tm 1; 1.

R Pfam; PR00001; 7tm 1; 1.

R PRINTS; PR00217; GPCR.
                                           ADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
                                                                                                      AVIVSIFGLCWAPYTLIMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
                                                                                                                                                                                                                                                                                                                                                   AVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFR
 MERAPPDGPLNASGALAGEAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
                                                                                                                                                 SSIPECHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
                                                                                                                                                                  SSIPEGHCYAEFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
                                                                                                                                                                                                            GPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSV
                                                                                                                                                                                                                             GPEPPFEAQPSPPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSV
                                                                                                                                                                                                                                                                      ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL
                                                                                                                                                                                                                                                                                       ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKOVVSQSFTQRFRLSRDRKVAKSL
                               ADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
                                                                                      SAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 445 AA; 48591 MW; E79440A4EC09CARC ERG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histamine receptor H3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.4%; Score 2323; DB 2; 98.2%; Pred. No. 2.4e-124; ive 2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $
                                                                                                                                                                                                                                                                                                                                                                                                        RAFTKLLCPQKLKIQPHSSLEHCWK 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01471; HISTAMINEH3R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=HRH3;
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SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA 240
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                                                                                                                                                        Coge F., Rique H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,
                                                                                                                                                                                                                                        241 GPEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLHRYGVGEAAAGAEAGETALGGGGGGGSA
                                                                                                                                                                                                                                                                                                             ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of mouse histamine H3 receptor.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The H3 subclass of histamine receptors could mediate thistamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist) (By similarity).
-!- SUBCELULIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Histamine H3 receptor (HH3R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445
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InterPro; IPR003980; H3_receptor.
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Pfam; PF00001; 7tm_1; 1
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MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
"High constitutive activity of native H3 receptors regulates histamine
                                                                                                                                                                                                                                                                                                                                                                          receptor.";
Mol. Pharmacol. 55:1101-1107(1999).
-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals thistough the inhibition of ademylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                   MEDLINE=20330707; PubMed=10869375;
Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
"Cloning of rat histamine H3 receptor reveals distinct species
pharmacological profiles.";
                                                                                                                                                                                                                                                                                                                        MEDLINE=99278519; PubMed=10347254;
Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).. Itadami H., Takkimura T., Nakamura T., Ohta M., "Cloning a novel g protein-coupled receptor."; submitted (JUN-1998) to the EMBL/GenBank/DbbJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            agonist).
SUBCELULAR LOCATION: Integral membrane protein.
SUBCRATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                         Pharmacol. Exp. Ther. 293:771-778(2000)
                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
            FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1; Synonyms=H3L;
IsoId=Q9QYN8-1; Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=2; Synonyms=H3S;
                                                                                                                                                                                                    neurons in brain.";
Nature 408:860-864(2000)
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                                                                                                                                   TISSUE=Striatum;
120
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                                                                                                                                                                                                                                                                      . .) (Potential)
                                                                                                                                                                                                                                                                                                           Score 2220; DB 1; Length 445; Pred. No. 1.7e-118;
                                                                                                                                                                                                                                                                                                                                       17; Indels
         PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                Potential.
Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                    48541 MW; B8D406E29E1F3C5F CRC64;
                                                  Extracellular (Potential) Potential.
                                                                                                      Extracellular (Potential) Potential.
                                                                                                                                                                                                                Extracellular (Potential)
                                                                                                                                                                                    Cytoplasmic (Potential). Potential.
                                                                                                                               Cytoplasmic (Potential).
                                                                              Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                      N-linked (GlcNAc.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 45, Last annotation update)
Histamine H3 receptor (HH3R).
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8; Mismatches
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Matches 419; Conservative
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445 AA;
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H13R RAT
ID H13R RAT
AC 090XN8; 09
DT 28-FEB-200
DT 28-FEB-200
DT 25-OCT-200
DT 18-EMB-100
C Name-H115; 05
Rattus nor
C Mammalia; 00
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                                                                                                                                             Isoid=Q9QYN8-4; Sequence=VSP_001888, VSP_001889;
TISSUE SPECIFICITY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform 1 is largely predominant in all tissues. MISCELLANEOUS: Proxyfan acts as a potent neutral antagonist while thioperamide, ciproxifan and FUBA65 act as potent inverse
                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
IsoId=Q9QYN8-2; Sequence=VSP_001887;
                                Name=3;
IsoId=Q9QYN8-3; Sequence=VSP_001888;
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RGD; 620630; Hrh3.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;

Rattus norvegicus (Rat)

Sequence=Displayed;

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CAVPO
                                                                             Name=HRH3;
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                                                                                                                                                                                                                                                                                                 WYETSFWLLWANSAVNPVLYPLCHYSFRRAFTKLLCPOKLK
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                                                                                                                                                                                                                                                                            Missing (in isoform 3 and isoform 4)
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                    PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                            N-linked (GlcNAc. . .) (Potential)
Missing (in isoform 2).
/FTId=VSP 001887.
                                                                                                                                                                                                                                                                                                                                                                                         Score 2213; DB 1; Length 445;
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                                                                  Extracellular (Potential)
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Cytoplasmic (Potential)
Poly-Ala.
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/FTId=VSP_0018
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                                                                                                                      Potential
                                                                                                                                                                                                                                                                                                                                                                   445 AA; 48588 MW;
GPCRRHODOPSN.
HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                                                                                        93.7%;
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Matches 417; Conservative
                                                                                                                                                                                                                                                                                                   445
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PR00237; C
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92
1109
1130
1130
1157
1178
1197
218
3360
3361
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20
11
274
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                                                     Transmembrane.
DOMAIN
TRANSMEM 4
DOMAIN 6
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TRANSMEM
DOMAIN
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TRANSMEM
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CARBOHYD
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                      Name=Long; Synonyms=H31;
Iso1d=094135-1; Sequence=Displayed;
Name=Short; Synonyms=H35;
Iso1d=094135-2; Sequence=VSP 001880;
TISSUE SPECIFICITY: Expressed widely and abundantly throughout the
Prain. Highly expressed in discrete neuronal populations such as
pyramidal cells in cerebral correx or cerebellar Purkinje cells.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                      -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
                                                                                                                                                                                                                                                                                                      histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                           Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                MEDIINE=20218440; PubMed=10757514;
Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C. Cochois V., Schwartz J.-C., Arrang J.-M.;
"Cloning and cerebral expression of the guinea pig histamine H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00001; 7tm 1; 1.
PRINTS: PR00231; GFCRRADODSN.
PRINTS: PR01411; HISTAMINEH3N.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.
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Potential.
Extracellular (Potential)
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Extracellular (Potential)
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Cytoplasmic (Potential).
Poly-Ala.
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Potential.
                                                                                                                                                                                                                                                                                                                                                             SÜBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
       SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
445 AA.
                                                                                                                                                                                                                                                           receptor: evidence for two isoforms.";
NeuroReport 11:755-759(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
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P14791
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PRINTS; PRO1471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 365 AA; 40609 MW; D78B32042464CB35 CRC64;
                                                                                                                     Score 1919; DB 2;
Pred. No. 1.8e-101;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AA
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                                                                                                                                                               Matches 365; Conservative
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                                                                                                                                            Similarity
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                                                                                                                           Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                            SLAIIVSIFGLCWAPYILLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHYS
                                                                                                                                                                                                        VADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCT
                                                                                                                                                                                                                                                                                          61 VADSSLRTQNNFFLLNLAISDFLVGVFCIPLYVPYVLJGRWTFGRGLCKIWLVVDYLLCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAK
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                                                                                                                                                                                 1 MERAPPDGPLNASGALAGD-AAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGPEPPPEAQPSPP-PPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGG
                                                                                                                                              Gaps
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-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity) 0:1-5 SUBCELLULAR LOCATION: Integral membrane protein coupled receptors. Integral paints and protein coupled receptors. Integral paints and protein coupled receptors. GO: GO:0016021; C:integral to membrane; IEA. GO: GO:0004959; F:intstamine receptor activity; IEA. GO: GO:0001584; F:receptor activity; IEA. GO: GO:0001584; F:rhodopsin-like receptor activity; IEA. GO: GO:0001587; F:receptor activity; IEA. GO: GO:0001587; F:receptor activity; IEA. Findopsin-like receptor protein signalin. ..; PRINTS; PRO0001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Hippocampus;
Wellendorph P.; Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
N-linked (GlcNAc. . .) (Potential)
Missing (in isoform Short).
/FTId=VSP_001880.
                                                                                                                                                4;
                                                                                                      Length 445;
                                                                                                    92.3%; Score 2179; DB 1; Length 4 92.8%; Pred. No. 3.7e-116; ive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weiner D.M.; "Molecular Cloning and Characterization of Functionally
                                                          48734 MW; BAE206A3887189A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Histemine H3 receptor isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoforms of the Human Histamine H3 Receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRRAFIKLLCPOKLKIOPHSSLEHCWK 445
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                                                                                                                     Best Local Similarity 92.8% Matches 415; Conservative
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                                                              445 AA;
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276
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    CARBOHYD
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AC 088WY
DT 01-M
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Isoforms of the Human Histamine H3 Receptor.";
Isoforms of the Human Histamine H3 Receptor.";
Neuropharmacology 0:0-0(2002).
-:- SIMILARITY Belongs to family 1 of G-protein (By similarity).
-:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL, AR31913; AAL71941.; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016059; F:histamine receptor activity; IEA.
GO; GO:0001894; F:rheceptor activity; IEA.
GO; GO:0001896; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001896; F:rhodopsin-like receptor protein signalin. .; IEA.
FFAm; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADSSLRTQNNFFILNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
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                                                                                                                                                                                                 1 MERAPPOGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
                                                                                                                                                                                                                                                                    ADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
                                                                                                                                                                                                                                                                                                                                                                                                      SAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL
                                                                                                                              1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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                                                               Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                           80,
Length 365;
                                                           0; Indels
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
11-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Histamine H3 receptor isoform 4.
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Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Q8N149;
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1. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AF31912; AAL71913.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:0004814; F:receptor activity; IEA.
GO; GO:0001884; F:rhidopsin.like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. ..; IEA.
                                                                                                                                           1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
                                                                                                                                                                                       61 ADSSLRTQNNFFILMAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
                                                                                                                                                                                                                                       SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAA
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                                                                                                                                                                              ADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS
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                                                                                                                              1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
                                                                                                         Gaps
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TISSUE-Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiner D.M.;
"Molecular Cloning and Characterization of Functionally Distinct Isoforms of the Human Histamine H3 Receptor.";
Neuropharmacology 0:00-0(2002)
                                                                                                         80;
                                                                                  Length 373;
                                                                                                       Indels
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-procein coupled receptor; Receptor; Transmembrane.
SEQUENCE 373 AA; 41570 MW; FAE9DFC5C3AF4DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                               Score 1919; DB 2;
Pred. No. 1.8e-101;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       301 AA
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                                                                                  81.3%;
82.0%;
                                                                                             Best Local Similarity 82.0
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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01-MAR-2002
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TISSUE-Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R.,
Pfam; PP00001; 7tm 1; 1.

PRINTS; PR01237; GFCRRHODOPSN.

PRINTS; PR01471; HISTAMINBH3R.

PROSITE; PS50024; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histamine H3 receptor isoform 6
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0
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                                                                                                                                                                           Score 1521; DB 2
Pred. No. 6e-79;
                                                                                                                                                             64.4%; bred. No. oc. 67.6%; Pred. No. oc. 7. Mismatches
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Nuzny D.D., Sodergene E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krozwinski M.I., Skalaka U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LITASTLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGGRE-AGPEPPPDAQPSPPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 CWGCWOKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSVASPTSSSGSSSRGTERP
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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 247;
                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO20847; AAH2847.1;
RGDJ; MGI:2139279; Hrh3.
RGD; MGI:2139279; Hrh3.
RGJ; GO:0016021; C:integral to membrane; TAS.
RINterPro; IPR000276; GPCR_Rhodpsn.
R Pfam; PF00001; Tru 1; 1.
R PRINTS; PR00237; GPCRHODOPSN.
R PRINTS; PR0171; HISTAMINEH3R.
R PROSTIE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.8%; Score 1223; DB 2; Length 2
91.5%; Pred. No. 4.2e-62;
ive 6; Mismatches 13; Indels
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
SI:bZ34G2.4 (Novel protein similar to human histamine
                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                 and mouse cDNA sequences.";
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Matches 227; Conservative
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                                                                                                                                                                                                                                                                     1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
                                                                                                                                                                                                                                    Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                  0; Indels 144;
   receptor protein signalin.
                                                                                                                                                                                                 Length 309;
                                                 Print Pronol; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR00471; HISTAMINEH3R.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 309 AA; 34242 MW; B7496F7D1D2A206B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GPEPPPEAQPSPPPPGCWGCWQKGHGEAMPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                               64.4%; Score 1521; DB 2; 67.6%; Pred. No. 6.2e-79; rative 0; Mismatches 0;
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GO, GO:0007186; P:G-protein coupled
Interpro, IPR00276; GPCR_Rhodpsn.
Interpro; IPR003980; H3_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                  Matches 301; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hrh3 protein (Fragment)
                                                                                                                                                                                            Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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Q8K116;
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61 FFNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLH-- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 GVGEAAVGAEAGEATLGGGGGGGSVASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEK
                                                                                                                                                                                                                                                                                                                                                                                                                   156 MLLVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLLVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 RMKMVSQSFTQRFRLSRDRKVAKSLAVIVSIFGLCWAPYTLLMIIRAACHGHCVPDYWYE
                                                                                                                                                                                                                                                                                                                                                                               80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brann M.R.,
 Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanaqi T., Ninomiya K.; Submirted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO74730; BAC11157.1; -.

EMBL, AKO74730; BAC11157.1; -.

EO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0001959; F:histamine receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001188; F:rhodopsin-like receptor protein signalin...

InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR000276; GPCR Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445
                                                                                                                                                                                                                                                                                                                                        48.2%; Score 1137; DB 2; Length 210; 72.4%; Pred. No. 2.8e-57; ive 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 TSFWLLWANSAVNPVLYPLCHHSPRRAFTKLLCPQKLKIQPHSSLEHCWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 TSFWLLWANSAVNPVLYPLCHHSFRRAFTKLLCPQKLKIQPHSSLEHCWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Hippocampus;
Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R.,
                                                                                                                                                                                                                                                                                                      210 AA; 24046 MW; 952F3FFD60077CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Histamine H3 receptor isoform S
                                                                                                                                                                                                                                                                   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                         Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 72.4
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                        Receptor.
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           요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 GCWQKGHGEAM-----PLHRYGVGEAAVGAEAGEATLGGGGGGGSVASPTSSSGSSSRG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EKRMKMVSQSFTQRFRLSRDRK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                      88
- I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

BRID. ALP28906. CAE49238.1.

ZFIN; ZDB-GRNE-040724-204; si:rp71-3492.4.

R GO; GO:0004962; F:histanine receptor activity; IEA.

R GO; GO:00049672; F:ricaptor activity; IEA.

R GO; GO:00049672; F:receptor activity; IEA.

R GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

R GO; GO:0001884; F:rhodopsin-like receptor protein signalin. . .; IEA.

R InterPro; IPR000376; GPCR_Rhodpsn.

InterPro; IPR0003980; H3 receptor.

R InterPro; IPR0003980; H3 receptor.

R PRINTS; PR00027; GPCR_RHODPsn.

R PRINTS; PR00171; H3TAMINEH3R.

R PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

R PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

R PROSITE; PS00237; GPROTEIN RECEP F1 2; Tansmembrane.

SEQUENCE 473 AA; 53506 WW; 032FC7C27D8C6E57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKRRDSTLADLPPLQVBERILAASEAQFHYVDHSAGFHRHRPDWVA-SLANRFRLSRDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAKSLAVIVSIPGLCWAPYTLIMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPFISVTYFNLSIYINIRNRCAMR-------EEQPTYVRLRSFKMKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                    29 FSAAWTAVLAALMALLIVATVLGNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                  . 99
                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                              86; Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ90249.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                           Query Match 50.2%; Score 1186; DB 2;
Best Local Similarity 54.2%; Pred. No. 9.5e-60;
Matches 240; Conservative 51; Mismatches 86
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|HSSFKRAFSKLLCPSKTKIQPQN 468
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QBNCH4;
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61 RFLSVTRAVSYRAQQGDTRRAVQKMVLVWVLAFLLYGPAILSWEHLSGGSSIPEGHCYAE 120
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16-0CT-2001 [Rel. 40, Last sequence update)
25-0CT-2004 [Rel. 45, Last annotation update)
Histamine H4 receptor (HH4R) (GPRv53) (G protein-coupled receptor 105)
(GPCR105) (SP9144) (AXOR35).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oda T., Morikawa N., Saito Y., Masuho Y., Mateumoto S.-I.; "Molecular cloning and characterization of a novel type of histamine receptor preferentially expressed in leukocytes."; J. Biol. Chem. 275:36781-36786(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monsma F.J. Jr.; "Cloning and characterization of a novel human histamine receptor."; J. Pharmacol. Exp. Ther, 296:1058-1066(2001).
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MEDLINE-211046456, PubMed=11181941;
MEDLINE-211046456, PubMed=11181941;
MOSTE K.L., Behan J. Laz T.M., West R.E. Jr., Greenfeder S.A.,
Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,
Gustafson B.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofetra C.L., Blevitt J., Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.; "Cloning and pharmacological characterization of a fourth histamine receptor (H4) expressed in bone marrow.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
"Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21106320; PubMed=11179436;
Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan Boyce K., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S., Bergsma D.J., Fitzgerald L.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Leukocyte;
MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
": ביבביי הייד Tanaka K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ochem. Biophys. Res. Commun. 279:615-620(2000)
                                                                                                                                                                                                                                                                                    390 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                               192 FFYNWYFLITASTLEFFTPFLSVTFFN 218
                                                                                                               121 FFYNWYFLITASTLEFFTPFLSVTFFN 147
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Pharmacol. 59:420-426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of a novel histamine
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
PubMed=11179434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor, HH4R."
                                                                                                                                                                                                                                                                                                          OSH3NB; OSGZOO;
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                                                                                                                                                                                                                                                                                    HH4R HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=HRH4;
                                                                                                                                                                                                                                                    HH4R_HUMAN
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                 36.4%; Score 860; DB 2; Length 200; 100.0%; Pred. No. 1.4e-41;
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95.9%; Pred. No. 1.2e-35;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                           PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 200 AA; 21612 MW; 2038D14BC186D1EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AA; 16900 MW; 67F6A741B518B54E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histamine receptor H3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AA
                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
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PRINTS; PR0023; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
      InterPro; IPR003980; H3_receptor.
                            Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100. Matches 170; Conservative
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Matches 141; Conservative
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EMBL, AB044934; BAB13698.1; --
EMBL, AB045370; BAB20091.1; --
EMBL, AF310797; AAG32052.1; --
EMBL, AF31230; AAK12081.1; --
EMBL, AF329449; AAK43542.1; --
EMBL, AF32955; AAL01684.1; --
EMBL, AJ298292; CAC83493.1; --
EMBL, AY136745; AAN01271.1; --
PIR, JC7566; JC7566.
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PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung, pancreas, skeletal muscle, prostate, small intestine, spleen, fetal liver and lymph node.

-InNUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

-INSCELLANEOUS: Does not bind diphenhydramine, loratadine, ranitidine, cimetidine and chlorpheniramine. Shows modest affinity for dimaprit, impromidine, clobenpropit, thioperamide, burimamide clozapine, immepip and imetit. The order of inhibitory activity was imetit > clobenpropit > burimamide > thioperamide, or inhiperamide or closenpropit behaves as a partial agonist, dimaprit and impromidine show some agonist activity while clozapine behaves as a full agonist. Thioperamide shows inverse agonism (enhances CAMP activity). The order of inhibitory activity of histamine > R(-)-alphamethylhistamine > R(-)-alphamethylhistamine > R(-)-alphamethylhistamine behave as full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
SUBCELLULAR LOCATION: Integral membrane protein.
SUBSCELEVENTY: Expressed primarily in the bone marrow and eosinophils. Shows preferential distribution in cells of immunological relevance such as T-cells, dendritic cells, monocytes, mast cells, neutrophils. Also expressed in a wide variety of peripheral tissues, including the heart, kidney, liver, writety of peripheral tissues, including the heart, kidney, liver,
"Identification of a histamine H4 receptor on human eosinophils - Role
                                                                                                                       Publ H.L. III, TReda S.R., Aronstam R.S.,
"cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The H4 subclass of histamine receptors could mediate t
histamine signals in peripheral tissues. Displays a significant
level of constitutive activity (spontaneous activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
                             in eosinophil chemotaxis.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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Cytoplasmic (Potential).
2 (Potential).
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GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004969; P:histamine receptor activity; NAS.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR008102; Histamnrecept_H4.
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                                                                                                                                                                                                                                                                                                                                                                              74; Gaps
                                                                                                                                                                                                                      (Potential).
                                                                                                                                                                  Cytoplasmic (Potential).

By similarity.
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
                                                                                                                                                                                                                                      S-palmitoyl cysteine (Potential).
A > V (in Ref. 1).
H -> R (in Ref. 1).
Q -> R (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                            Length 390;
                                                                                                                                                                                                                                                                                                                                         30.7%; Score 724; DB 1; Length 39.38.6%; Pred. No. 1.4e-33; ive 56; Mismatches 131; Indels
                                                                                                             6 (Potential).
Extracellular (Potential).
7 (Potential).
Extracellular (Potential)
                                                4 (Potential).
Extracellular (Potential)
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                                                                                  5 (Potential).
Cytoplasmic (Potential).
                                 Cytoplasmic
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                                                                                                                                                                                                                                                                                                            44495 MW;
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 253 ;
390 AA;
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Evaluader, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT PILIG DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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OY 2641 AACCGTGAGGTCACAATAAAGTGTATTTTTTAAAAAAAAA	RES				TYPE: DNA ORGANISM: Artificial Sequence FEATURE:	; OTHER INFORMATION: Description US-09-642-514-5 Query Match 100.0%;	Best Local Matches 26		Db 61	Oy 121 CCGCCTGCTCTGGCCCCGGCCCCGGGGGCCTTGGGGCGCCCCGGGGGAA Db 121 CCGCCTGCTCTGGCCCCGGCCCCGGGGGCGCGTTGGGCTTGGGCGCCCCGGGGAAC	0 181 ACCCGACCCGGCCAAGGCCCGCAAAGACGAGGCTCCCGGGCCGGGCCCCTCCCGGGCCGGCGGGCCCTCCCGGCCGGAAAGACGAAGGCCCGGAAAGACGAGGCTCCCGGGAAAGACCAGGGCTCCCGGAAAGACGAGGCTCCCGGGAACGCCCGGAAAGACGAGGCTCCCGGGAGCCCCCCCC	QY 241	Db 241 Qy 301	Db 301	Oy 36.1 GOCGGCGGGGGGGGGGGGGTTTCTCGGCTGGACGCGGGTGCTGGCGGGGTCTAT 0 11.1111111111111111111111111111111111	Qy 421	Db 421	0 481 CGACTCGGACCTCCGAACAACATCTTCCTGGTCGACCTCGCCATCTTCCTCGCATCTTCCACCTTTTTTCTCGCAATCTTCCTGGTCAACTTCGAATTTCTTCCTGCTCAACTTCTCCAACTTCTTCCAACTTCCAACTTCTCCAACTTCTT	
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
AND AND AND AND AND AND AND USES THEREFOR TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
CARRESDESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
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Pred. No. 0;
0; Mismatches
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NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
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Best Local Similarity 99.6
Matches 2659; Conservative
                                                                                                                                                                      CITY: Boston STATE: Massachusetts
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STRANDEDNESS: single
TOPOLOGY: linear
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US-08-985-090-1
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                                                                                                                                                                                                  Sequence 1, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: ANDERED D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.6%; Score 2635:2; Best Local Similarity 99.8%; Pred. No. 0; Matches 2659; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Blizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 Date pairs
                                                                                             2656 ATTTTTTAAAAAAAAAAAAA 2679
                                                                2665 ATTTTTTAAAAAAAAAAAAAA 2688
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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; LOCATION: 291..1625
US-09-165-543-1
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US-09-165-543-1
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        CTCTCCCCGGACAAGCCCAGGACACTTTGCTGCCTTCTGTCTTGCATAAGCCTC
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        CTCTCCCCGGACAAGCCCAGGACACTGCCTTTGCTGCCTTCTGTCTTGCATAAGCCTC
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    1817 CTGGCTGGACTGGAGGCTGGGTGGCCGGCCCTGCCCCCCACATTCTGGCTCCACC-GGGA
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	RESULT 6 US-09-949-016-5059 US-09-949-016-5059 Sequence 5059, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITHOUT OF 1200-04-14 PRIOR PPLICATION NUMBER: 60/241,755 PRIOR PPLICATION NUMBER: 60/231,768 PRIOR PILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-08 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SEQ ID NO 5059 LENGTH: 2665 TTYPE: DNA TYPE: DNA CREANISM: Human US-09-949-016-5059	Query Match 97.64; Score 2633.6; DB 4; Length 2665; Best Local Similarity 99.8; Pred. No. 0; DB 4; Indels 2; Gaps 2; Matches 2658; Conservative 0; Mismatches 4; Indels 2; Gaps 2; Qy 10 Caccacracacracacracacracacracacracacrac

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Sequence 16801, Application US/09949016

Sequence 16801, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION: Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTESQ for Windows Version 4.0

SEQ ID NO 16801
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    2522 CAGGGCCGGTCCAGAGGAGGTGCCCGGGCCAGGGGCCGCTTCGCCATGTGCTGTGCACCCG 2581
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                                  TGCCACGCGCTCTGCATGCTCCTCTGCCTGTGCCCGCTGCGCTGCCCTGCAAACCGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%; Score 1947.8; 98.8%; Pred. No. 0; ive 0; Mismatches
                                                                                           GTCACAATAAAGTGTATTTTTTA 2673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.2
Best Local Similarity 98.8
Matches 1972; Conservative
                                                                                                                                                                    RESULT 7
US-09-949-016-16801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16801
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Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
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MEDIUM TYPE: Floppy disk
COMPUTER: Flam Pr. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: 33,505
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER ISTICS:
LENGTH: 3244 base pairs
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                                                                                               Length 3244;
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                                                                                                Score 1384.8; DB 3;
Pred. No. 1.2e-258;
0; Mismatches 632;
                                                                                                Query Match 51.3%;
Best Local Similarity 74.2%;
Matches 2043; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PERTURE:
                                                           CDS
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                                                         ; NAME/KEY:
; LOCATION:
US-09-165-543-4
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PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 21
LENGTH: 2050
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.3
Matches 1361; Conservative
                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (271)...(1629)
US-09-891-053-21
                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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Fatent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadami, Hiraku
APPLICANT: Tathmura, Teteuo
APPLICANT: Tathmura, Teteuo
APPLICANT: Robayashi, Masahiko
APPLICANT: Robayashi, Masahiko
APPLICANT: Anaka, Ken-ichi
APPLICANT: Tataka, Yusuke
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APPLICANT: Ohta, Masataka
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1111 GCTGCACAGGTATGGGGTGAGGCGGCCGTAGGCGCTGAGGCCGGGGAGGCGACCCT 1170	1171 CGGGGGTGGCGGTGGGCTCCGTGGCTTCACCCACCTCCAGCTCCGGCAGCTCCTC 1230 	1211 GAGGGCACTGAGAGGCGGCTCACTCAAGAGGGGCTCCAAGCGTCGTCGGCTCCTCGGC 1290 	1291 CTCGCTGGAGÀAGCGCATGAAGATGGTCCCAGAGCTTCACCCAGCGCTTTCGGCTGTC 1350 	1351 TCGGGACAGGAAAGTGGCCAAGTCGCTGGCCGTCATCGTGAGCATCTTTGGGCTCTGCTG 1410 	1411 GGCCCCATACACGCTGATGATCATCCGGGCCGCCTGCCATGGCCACTGCGTCCCTGA 1470 	1471 CTACTGGTACGAAACCTCCTTCTGGTCGTCGGCCAACTCGGCTGTCAACCCTGTCCT 1530 	1531 CTACCTCTGTGCCACCACAGCTTCCGCCGGGCCTTCACCAAGCTGCTCTGCCCCCAGAA 1590	1591 GCTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAA 1632 	ULT 11 09-167-354-6	atent No. 613659 ENERAL INFORMATION: APPLICANT: Lovenberg, Timothy	APPLICANT: ETLANDEI, MAIK APPLICANT: Pyati, Jayashree APPLICANT: Huvar, Arne TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3	FILE OF INVENTION: SUBTIVE FILE REPRENCE: JWW CURRENT APPLICATION NUMBER: US/09/167,354A MATTER OF FILING DATE: 1998-10-07	SOFTWARE: Patentin Ver. 2.0 EQ ID NO 6 EM 1335	ONEANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:CDNA	335;	SGCGGCGATGCG 35	

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US-09-642-514-6
Sequence 6, Application US/09642514
Patent No. 6437100:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Brander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
APPLICANT: Wash
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                                                                                                                                                                                                                                                                      Sequence 6, Application US/09642855
; Patent No. 641374:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
TITLE OF INVENTION: BUA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT APPLICATION NUMBER: 09/167,354
PRIOR PILING DATE: 1998-10-06
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; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6
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                                                                                                                                       GAGCACTGCTGGAAG 1633
                                                                                                                                                                           1321 GAGCACTGCTGGAAG 1335
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Matches 1335, Conservative
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US-09-642-855-6
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       961 AAGAGGGGTCCAAGCCGTCGGCGTCCTCGGCCTCGGAGAAGCGCATGAAGATGGTG
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Patent No. 5885893
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/985,090
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNI-032
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ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silverri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)22-7400
TELEFRAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
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COUNTRY: USA
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APPLICATION NUMBER:
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Best Local Similarity 100.0%; Pred. No. 4.1e-249;
Matches 1335; Conservative 0; Mismatches 0;
FILE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT FILING DATE: 2000-08-21
FRIOR APPLICATION NUMBER: US 09/167,354
FRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENT NET. 2.0
SOFTWARE: PALENT NET. 2.0
LENGTH: 1335
                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY.
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NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617)727-7400
TELEFRA: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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Patent No. 6093545
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Pred. No. 1.7e-248;
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Best Local Similarity 99.9%;
Matches 1333; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1..1335
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Search completed: June 2, 2005, 14:45:48
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Pred. No. 1.7e-248;
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Best Local Similarity 99.5
Matches 1333; Conservative
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STRANDEDNESS: sinc
TOPOLOGY: linear
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; LOCATION: 1..1335
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1 MERAPPDGPLNASGALAGDA......LLCPQKLKIQPHSSLEHCWK 445
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Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 11, Appli Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 7, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 16, Appli	MINE RECEPTOR OF THE H3	151; 0; Indels 0; Gaps 0; VLAALMALLIVATVLGNALVMLAFV 60 VLAALMALLIVATVLGNALVMLAFV 60 LTGRWTFGRGLCKLMLVVDYLLCTS 120 LTGRWTFGRGLGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
PCT-US93-08528-9 US-09-826-509-515 US-08-313-553-9 US-08-194-338-1 US-08-194-338-1 US-08-194-338-4 US-08-194-338-4 US-09-825-923-2 US-09-825-923-2 US-09-825-923-2 US-09-825-923-2 US-09-118-270-12 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5 US-08-194-338-5	ALIGNMENTS 354A G A HUMAN HISTA 09/167,354A of Artificial	; Score 2361; D ; Pred. No. 3.7e 0; Mismatches DAAAAGARGFSAAWTA DAAAAGARGFSAAWTA SDFLVGAFCIPLYVPYV SUFINITION
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28 29 30 31 31 31 31 31 31 31 31 31 449 470 470 470 470 470 470 470 470	RESULT 1 US-09-167-354-7 Sequence 7, Applicati Fetent No. 613659; GENERAL INFORMATION: APPLICANT: Elander, APPLICANT: Elander, APPLICANT: Patt, Ja APPLICANT: Patt, Ja APPLICANT: PATT, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: JWW CURRENT FILING DATE: NUMBER OF SEQ ID NOS SOFTWARE: PATT CURRENT FILING DATE: SEQ ID NO 7 LENGTH: 445 FEATURE: PATT ORGANISM: ARTIficia FEATURE: CORGANISM: ARTIFICIA	Matches Matches Matc

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RESULT 3
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                                                                                                                                                                                  Sequence 7, Application US/09642855
Patent No. 641374
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOVenberg, Timothy
APPLICANT: Fyai, Jayashree
APPLICANT: Pyai, Jayashree
TITLE OF INVENTION: BUR ENCODING A HUMAN HISTAMINE RECEPTOR OF THE
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 1998-10-06
PRIOR PRILING DATE: 1998-10-06
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO
LENGTH: 445
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Best Local Similarity
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                                                                                                        APPLICANT: Extander, Mark

APPLICANT: Extander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Ann

TITLE OF INVENTION: SUBTYPE

CURRENT APPLICATION NUMBER: US/09/642,514

CURRENT APPLICATION NUMBER: US 09/167,354

PRIOR APPLICATION NUMBER: US 09/167,354

PRIOR PILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

LENGTH: 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08985090
Patent No. 589E893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION:
MUNCHER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.7e-161;
Matches 445; Conservative 0; Mismatches 0;
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Sequence 7, Application US/09642514
Patent No. 6437100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                        GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
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GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
CORFESE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/09/165,543
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: protein US-09-165-543-2
                                                                                                                     CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 7.2e-161;
Matches 444; Conservative 1; Mismatches 0; Indels
                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
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 LLP
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NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE FOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
ADDRESSEE: LAHIVE & COCKFIELD, STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 445 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617)227-740
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-985-090-2
                            STATE: Massachusetts
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                    COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                            GPEPPPEAQPSPPPPPGCWGCWQKGHGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFTQRFRLSRDRKVAKSL
                                           Gaps
                                           ö
99.8%; Score 2357; DB 3; Length 445; 99.8%; Pred. No. 7.2e-161; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.8
Matches 444; Conservative
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RESULT 5 US-09-165-543-2 ; Sequence 2, Application US/09165543 ; Patent No. 609345

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RESULT 8
US-09-165-543-5
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                          FARENAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/237,768

PRIOR PELICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10930
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99.8%; Pred. No. 7.3e-161;
tive 1; Mismatches 0;
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Sequence 10930, Application US/09949016
Patent No. 6812339
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US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 675032;
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Nakamura, Takao
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Best Local Similarity 99.8'
Matches 444; Conservative
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US-09-949-016-10930
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APPLICANT: Haudra, Near-Aut.
APPLICANT: Haddar, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/691,053
CURRENT FILING DATE: 2001-09-17
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-25
PRIOR FILING DATE: 1999-12-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
SOFTWARE: PABLICATION NUMBER: JP 11/145661
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Patent No. 6093545

GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 453
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99.8%; Pred. No. 7.3e-161;
iive 1; Mismatches 0;
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Best Local Similarity 99.8
Matches 444; Conservative
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STATE: Massachusetts
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CORGANISM: Homo sapiens
US-09-891-053-20
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Score 2213; DB 4; Length 4
Pred. No. 1.4e-150;
9; Mismatches 18; Indels
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Kobayashi, Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.5%;
Matches 417; Conservative
               Tanaka, Ken-ichi
Hidaka, Yusuke
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT CRGANISM: Rattus norvegicus US-09-891-053-25
                                                                                                                                                                                                                                                                                                                              LENGTH: 445
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     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION DATA:
PILING DATE:
                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REGISTRATION NUMBER: MIL-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-7400
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APPLICATION NUMBER: 09/042,780
FILING DATE:
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Patent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadani, Hiraku
APPLICANT: Takimura, Teteno
APPLICANT: Nakamura, Takao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 93.5
Matches 417; Conservative
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                                                                                                                                                          CLASSIFICATION:
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US-09-891-053-25
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SAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
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APPLICANT: Ohter Masters APPLICANT: ON INVENTION: NOVEL GIANOSINE TRIPHOSPHATE (GTP) TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS FILE REPERENCE: 06501-093001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 1099-109-17
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-25
PRIOR FILING DATE: 1999-12-25
PRIOR FILING DATE: 1999-12-25
PRIOR PLUMG DATE: 1999-12-25
PRIOR PELING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayanahi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Wasataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
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239

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204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 -----SGGSSSRGTERPRSLKRGSKPSASSASLEKRMKWVSQSITQRFRLSRDKKVAKS 327
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                                                                                                                                                                                                                                                                                                                             Length 413;
                                                                                                                                                                                                                                                                                                                           Query Match 87.1%; Score 2057; DB 4; Best Local Similarity 87.9%; Pred. No. 1.8e-139; Matches 392; Conservative 8; Mismatches 12;
             CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT APPLICATION NUMBER: PCT/UP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/UP98/05967
PRIOR APPLICATION NUMBER: PCT/UP98/05967
PRIOR APPLICATION NUMBER: JP1/145661
PRIOR PLING DATE: 1999-12-25
PRIOR PLING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PSGESEQ for Windows Version 4.0
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                         US-09-891-053-1
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61 AQQGDTRRAVRXMALVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLISAS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 PKGHGEAMPLHRYGVGEAGPGVEAGEAALGGGSGGGAAASPTSSSGSSSRGTERPRSLKR 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAFCIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.4%; Score 1828; DB 2; Length 362; 92.8%; Pred. No. 3.8e-123; tive 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: LAHIVE & COCKFIELD, LLP 28 State Street
                                                                                                                                    PRICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-CTELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 92.8
Matches 337; Conservative
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MOLECULE TYPE: protein
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STATE: Massachusetts
COUNTRY: USA
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US-09-165-543-32
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Gaps

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107 SAFNIVLISYDRFLSYURAVSYRAQQGDTRRAVRKMLLVWVLAFLLYGPAILSWBYLSGG 166
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                                                                                                                                               1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV
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                                                                                                         94;
                                                                 Length 351;
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38.6%; Pred. No. 3.3e-44;
tive 56; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 GPEPPEAQPSPPPPGCWGCWQKGHGEAMPLH--------
                                                                                                       Indels
                                                               77.1%; Score 1820; DB 3; 78.7%; Pred. No. 1.4e-122; iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Morse, Kelley L.
APPLICANT: Wang, Suke
APPLICANT: Wang, Suke
TILLE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 RAFTKLLCPQKLKIQPHSSLEHCWK 445
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Patent No. 6204017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 38.6
Matches 164; Conservative
                                                                 Query Match 77.1
Best Local Similarity 78.7
Matches 350; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens
        ORGANISM: HOMO SAPIENS
            ; UKGANISM: EX
US-09-524-162-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLEFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPFEAQPSPPP-PPGCWGCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
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APPLICANT: Ping TBUI
TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
FILE REFERENCE: GP-70681
CURRENT APPLICATION NUMBER: US/09/524,162
CURRENT PILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 351
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.4%; Score 1828; DB 3;
92.8%; Pred. No. 3.8e-123;
tive 8; Mismatches 16;
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFISENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09524162
Patent No. 6355452
                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.4
Best Local Similarity 92.8
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-165-543-32
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                   FILING DATE:
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US-09-524-162-2
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Search completed: June 2, 2005, 20:41:49
Job time : 29 secs
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                                                                                                     EFFTPFLSVTFPNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPGCWGCWQKG 265
                                                                                                                        HGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
                                                                                                                                                                                                                                          150 RRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFYNWYFLITASTL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFFTPFLSVTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPGCWGCWQKG 265
206 HLSRCQSH------PGLTAVSSNICGHSFRGRLSSRRSLSASTEVPASFHSRRRRX 257
                                                                                                                                                                                                                                                                                 PYTILIMIIRAACHGHCVP-DYWYETSFWILWANSAVNPVLYPICHHSFRRAFTKLLCPQK 431
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                                            11 SLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAISDFFVGUSIP
                                                                                                                                                                                                                        SLKRGSKPSASSASLEKRMKMVSQSFT-----QRFRLSRDRKVAKSLAVIVSIFGLCWA
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30.7%; Score 724; DB 4; Length 390
Best Local Similarity 38.6%; Pred. No. 3.3e-44;
Matches 164; Conservative 56; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Kelley L.
APPLICANT: Wang, Shelby P.
APPLICANT: Wang, Shelby P.
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
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Patent No. 6613533
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ORGANISM: Homo sapiens
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PYTLLMIIRAACHGHCVP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKLLCPQK 431
                                                                                                                                                                     26 HGEAMPLHRYGVGEAAVGAEAGEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
                                                                          SLKRGSKPSASSASLEKRMKMVSQSFT-----QRFRLSRDRKVAKSLAVIVSIFGLCWA
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375 IKKQP 379
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